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OM protein - protein search, using sw model

Run on: October 29, 2002, 09:31:07 : Search time 30 Seconds

(without alignments)
37.025 Million cell updates/sec

Title: US-09-724-842A-27
Sequence: 1 HHOKLVFAE 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 135323

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
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21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	22	AAAB6225 Human APP derived
2	52	94.5	10	22	AAAB2641 All-D peptide used
3	50	90.9	9	22	AAAB4893 Antifibrillogenic
4	50	90.9	10	22	AAAB6224 Human APP derived
5	47	85.5	10	22	AAAB6226 Human APP derived
6	46	83.6	8	18	AAW45937 Amyloid beta pepti
7	46	83.6	9	18	AAW45935 Amyloid beta pepti
8	46	83.6	10	18	AAW45934 Amyloid beta pepti
9	42	76.4	10	22	AAAB6223 Human APP derived
10	42	76.4	8	17	AAW02310 Beta-amyloid modul
11	42	76.4	8	20	AAW89374 Beta-amyloid pepti

12	40	72.7	7	18	AAW45941
13	40	72.7	8	18	AAW45938
14	40	72.7	9	18	AAW45936
15	40	72.7	10	22	AAAB6222
16	39	70.9	10	22	AAAB6227
17	38	69.1	7	14	AAW45231
18	38	69.1	7	17	AAW02311
19	38	69.1	7	18	AAW45940
20	38	69.1	7	14	AAW89375
21	36	65.5	9	20	AAW45239
22	34	61.8	6	18	AAW45946
23	34	61.8	7	14	AAW45232
24	34	61.8	7	16	AAW87921
25	34	61.8	7	16	AAW88300
26	34	61.8	7	16	AAW80370
27	34	61.8	7	17	AAW02312
28	34	61.8	7	18	AAW45942
29	34	61.8	7	19	AAW49755
30	34	61.8	7	20	AAW89376
31	34	61.8	7	22	AAW67281
32	34	61.8	8	18	AAW45939
33	34	61.8	8	18	AAW32551
34	34	61.8	8	22	AAE10663
35	34	61.8	8	22	AAE02615
36	34	61.8	10	21	AAW79938
37	34	61.8	10	22	AAW46221
38	34	61.8	10	22	AAW46228
39	32	58.2	6	18	AAW45945
40	31	56.4	7	14	AAW45233
41	31	56.4	7	22	AAW82639
42	31	56.4	7	22	AAW82640
43	31	56.4	7	22	AAW46491
44	31	56.4	7	22	AAW46492
45	30	54.5	5	18	AAW45952
46	30	54.5	6	17	AAW02313
47	30	54.5	6	18	AAW45947
48	30	54.5	6	18	AAW45944
49	30	54.5	6	20	AAW39801
50	30	54.5	6	20	AAW29090

ALIGNMENTS

RESULT 1
AAB46225 standard; peptide; 10 AA.
AAB46225;
04-APR-2001 (first entry)
Human APP derived immunogenic peptide #21.
Amyloid deposit; APP, Abeta; brain; human; clearing response; nootropic;
Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
amyloid precursor protein; Alzheimer's disease.

Homo sapiens.

WO200072880-A2

07-DEC-2000. *plaster 11-29-00*

26-MAY-2000; 2000WO-0514810.

28-MAY-1999; 99US-0322289.

(NEUR-) NEURALAB LTD.

Schenk DB, Bard F, Vasquez NJ, Yednock TJ;

WPI; 2001-032104/04.

Amyloid beta pepti
Amyloid beta pepti
Amyloid beta pepti
Human APP derived
Beta amyloid prote
Beta-amyloid modul
Amyloid beta pepti
Mutant amyloid pre
Amyloid beta pepti
Beta amyloid prote
Test peptide used
Non-amnesic pepti
Protein polymeric
Beta-amyloid modul
Amyloid beta pepti
Glutamine donor pe
Beta-amyloid pepti
Residues 16-22 of
Amyloid beta pepti
Amyloidogenic sequ
Human amyloid prec
Human amyloid prec
Beta-amyloid recog
Human APP derived
Human APP derived
Amyloid beta pepti
Beta amyloid prote
All-D peptide used
All-D peptide used
Antifibrillogenic
Antifibrillogenic
Amyloid beta pepti
Beta-amyloid modul
Amyloid beta pepti
Beta-amyloid pepti
Beta-amyloid prote
A-beta-binding pep

Piles
600/50 70880

search up front by function

XX Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX
 PS Disclosure; Figure 19; 143pp; English.
 XX
 CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 CC
 SO Sequence 10 AA;
 OY 1 HHOKLVFFAE 10
 DB 1 HHOKLVFFAE 10
 Query Match 100.0%; Score 55; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 2
 AAB82641
 ID AAB82641 standard; Peptide; 10 AA.
 AC AAB82641:
 DT 02-OCT-2001 (first entry)
 XX
 DE All-D peptide used in Alzheimer's disease vaccine.
 XX
 KW Alzheimer's disease; amyloidosis; amyloid-related disease;
 KM vaccine; therapy; antigen.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 1..10 /note- "all D-form residues"
 XX
 PN WO200139796-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 29-NOV-2000; 2000MO-CA01413.
 XX
 PR 29-NOV-1999; 99US-0168594.
 PR 28-NOV-2000; 2000US-0724842.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Chalfour R, Hebert L, Kong X, Gervais F;
 DR WPI; 2001-441458/47.
 XX
 PT Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, e.g. as
 PT vaccine, which elicits production of antibodies to prevent
 PT fibrillogenesis and associated cellular toxicity -
 XX
 PS Disclosure; Page 11; 31pp; English.
 XX

CC The present sequence is that of an all-D peptide suitable for
 CC use in preparing vaccines for preventing or treating Alzheimer's
 CC disease and other amyloid related disorders in humans. It is based
 CC on a portion of amyloid-beta peptide (see AAB82622), and may be
 CC modified by removing or inserting 1 or more amino acid residues, or
 CC by substituting 1 or more amino acid residues with other amino acid
 CC residues or non-amino acid fragments. Vaccines of the invention
 CC are produced using 'non-self' peptides synthesised from the
 CC unnatural D-configuration amino acids to avoid the drawbacks of
 CC 'self' proteins. The all-D peptides need not be aggregated to be
 CC operative or immunogenic. They preferably interact with at
 CC least 1 region of an amyloid protein, e.g. the beta-sheet region
 CC or GAG-binding site region, the amyloid-beta peptide, or their
 CC immunogenic fragments, protein conjugates, immunogenic derivative
 CC peptides and immunogenic peptidomimetics. Examples include all-D
 CC peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,
 CC 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D
 CC derivative peptides given in AAB82623-64. The vaccine elicits a
 CC preferential TH-2 or TH-1 response, preventing fibrillogenesis and
 CC associated cellular toxicity. The amyloid related diseases may be
 CC diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob
 CC disease, scrapie, cerebral amyloid angiopathy, and prion protein
 CC related disorders, or systemic amyloidosis associated with chronic
 CC infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and
 CC systemic amyloidosis found in long-term haemodialysis patients.
 CC
 SO Sequence 10 AA;
 OY 1 HHOKLVFFAE 10
 DB 1 HHOKLVFFAE 10
 Query Match 94.5%; Score 52; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.00056;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 AAB48493
 ID AAB48493 standard; Peptide; 9 AA.
 AC AAB48493:
 DT 02-MAR-2001 (first entry)
 XX
 DE Antifibrillogenic peptide #20.
 XX
 KW Neurotropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KM cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KM Alzheimer's disease.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Modified-site 9 /note- "C-terminal amide"
 XX
 PN WO200068263-A2.
 XX
 PD 16-NOV-2000.
 XX
 PF 04-MAY-2000; 2000MO-CA00515.
 XX
 PR 05-MAY-1999; 99US-0132592.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Chalfour R, Gervais F, Gupta A;
 DR WPI; 2001-031852/04.
 XX

PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic -
 XX
 XX
 PS Claim 7; Page 25; 46pp; English.
 CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are
 CC therefore useful for treating amyloidosis disorders such as Alzheimer's
 CC disease. Peptides AAB48474-B48496 were identified from the
 CC glycosaminoglycan binding region and the prot-prot interaction region of
 CC the human amyloid protein.
 XX
 XX
 SQ Sequence 9 AA;
 Query Match 90.9%; Score 50; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HOKLVFFA 9
 DB 1 HOKLVFFA 9
 RESULT 4
 ID AAB46224 standard; peptide; 10 AA.
 AC AAB46224;
 DT 04-APR-2001 (first entry)
 DE Human APP derived immunogenic peptide #20.
 XX
 XX Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KM Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KM amyloid precursor protein; Alzheimer's disease.
 XX
 OS Homo sapiens.
 PA WO200072880-A2.
 PN 07-DEC-2000.
 PD 26-MAY-2000; 2000WO-US14810.
 PF 28-MAY-1999; 99US-0322289.
 PR (NEUR-) NEURALAB LTD.
 PA Schenk DB, Bard F, Vasquez NJ, Yednock T;
 PI WPI; 2001-032104/04.
 DR Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX
 PS Disclosure; Figure 19; 143pp; English.
 CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of

CC Alzheimer's disease.
 XX
 SQ Sequence 10 AA;
 Query Match 90.9%; Score 50; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HOKLVFFA 9
 DB 2 HOKLVFFA 10
 RESULT 5
 ID AAB46226 standard; peptide; 10 AA.
 AC AAB46226;
 DT 04-APR-2001 (first entry)
 DE Human APP derived immunogenic peptide #22.
 XX
 XX
 DE Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KM Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KM amyloid precursor protein; Alzheimer's disease.
 XX
 OS Homo sapiens.
 PA WO200072880-A2.
 PN 07-DEC-2000.
 PD 26-MAY-2000; 2000WO-US14810.
 PF 28-MAY-1999; 99US-0322289.
 PR (NEUR-) NEURALAB LTD.
 PA Schenk DB, Bard F, Vasquez NJ, Yednock T;
 PI WPI; 2001-032104/04.
 DR Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX
 PS Disclosure; Figure 19; 143pp; English.
 CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 XX
 SQ Sequence 10 AA;
 Query Match 85.5%; Score 47; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HOKLVFFA 10
 DB 1 HOKLVFFA 9

```

RESULT 6
ID AAM45937 standard; peptide; 8 AA.
XX
XX AAM45937;
XX
DE 30-JUN-1998 (first entry)
XX
DE Amyloid beta peptide fragment.
XX
DE Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
XX position emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS Homo sapiens.
XX
PN M09721728-A1.
XX
PD 19-JUN-1997.
XX
PE 09-DEC-1996; 96WO-SE01621.
XX
PR 29-DEC-1995; 95US-0009386.
XX PR 12-DEC-1995; 95SE-0004467.
XX
PA (KARO-) KAROLINSKA INNOVATIONS AB.
XX
PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
DR WPI; 1997-332723/30.
XX
PT Use of new and known peptide(s) for inhibition of polymerisation of
XX amyloid beta peptide e.g. for treatment of Alzheimer's disease or
XX Down's syndrome associated with amyloidosis.
XX
PS Example 1; Figure 2B; 31pp; English.
XX
CC This sequence represents a fragment of the amyloid beta peptide. The
XX invention relates to the use of peptide compounds for inhibition of
XX polymerisation of amyloid beta peptide (ABP), as model substances for
XX synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
XX tool for the identification of other organic compounds with similar
XX functional properties, or as ligands in positron emission tomography.
XX The peptides may be used in treatment of amyloidosis, especially in
XX treatment of Alzheimer's disease associated with amyloidosis, for
XX treatment or prevention of dementia in patients with Down's syndrome, for
XX treatment or prevention of hereditary cerebral haemorrhage with
XX amyloidosis (Dutch type) or for the prevention of fibril formation of
XX human amyloid protein. They can also be used for identifying other
XX molecules with similar properties and/or as ligands for detection of
XX amyloid deposits using e.g. positron emission tomography.
XX
SQ Sequence 8 AA;
XX
QY Query Match 83.6%; Score 46; DB 18; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 6.4e+05;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 HHOKLVEF 8
XX I HHOKLVEF 8
XX | |||||
XX | |||||
XX | |||||
XX Db 1 HHOKLVEF 8
XX
RESULT 7
ID AAM45935 standard; peptide; 9 AA.
XX
XX AAM45935;
XX AC
XX 08-JUL-1998 (first entry)
XX
XX Amyloid beta peptide fragment.
XX

```

KW		Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KM		positron emission tomography; PET; Down's syndrome; amyloidosis.
XX	OS	Homo sapiens.
XX	PN	MO9721728-A1.
XX	PD	19-JUN-1997.
XX	PF	09-DEC-1996; 96WO-S01621.
XX	PR	29-DEC-1995; 95US-0009386.
XX	PR	12-DEC-1995; 95SE-0004467.
XX	PA	(KARO-) KAROLINSKA INNOVATIONS AB.
XX	P1	Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
XX	DR	WP1: 1997-332723/30.
XX	PT	Use of new and known peptide(s) for inhibition of polymerisation of
XX	PT	Amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
XX	PT	Down's syndrome associated with amyloidosis.
XX	PS	Example 1; Figure 2B; 31pp; English.
XX	CC	This sequence represents a fragment of the amyloid beta peptide. The
XX	CC	invention relates to the use of peptide compounds for inhibition of
XX	CC	polymerisation of amyloid beta peptide (ABP), as model substances for
XX	CC	synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
XX	CC	tool for the identification of other organic compounds with similar
XX	CC	functional properties, or as ligands in positron emission tomography.
XX	CC	The peptides may be used in treatment of amyloidosis, especially in
XX	CC	treatment of Alzheimer's disease associated with amyloidosis, for
XX	CC	treatment or prevention of dementia in patients with Down's syndrome,
XX	CC	for treatment or prevention of hereditary cerebral haemorrhage with
XX	CC	amyloidosis (Dutch type) or for the prevention of fibril formation of
XX	CC	human amyloid protein. They can also be used for identifying other
XX	CC	molecules with similar properties and/or as ligands for detection of
XX	CC	amyloid deposits using e.g. positron emission tomography.
SQ	Sequence	9 AA:
QY	Query Match	83.6%; Score 46; DB 18; Length 9;
	Best Local Similarity	100.0%; Pred. No. 6.4e+05;
Matches	8; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	1 HHOKLVEF 8	
	2 HHOKLVEF 9	
RESULT 8		
AAW45934		
ID AAW45934	standard; peptide; 10 AA.	
AC AAW45934;		
XX		
DT 08-JUL-1998	(first entry)	
DE	Amyloid beta peptide fragment (residues 11-20).	
XX		
KM	Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;	
KW	positron emission tomography; PET; Down's syndrome; amyloidosis.	
XX	Homo sapiens.	
XX		
XX	MO9721728-A1.	
XX		
XX	PD	19-JUN-1997.
XX	PF	09-DEC-1996; 96WO-S01621.

PR 29-DEC-1995; 95US-0009386.
 PR 12-DEC-1995; 95SE-0004467.
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
 DR WPI; 1997-332723/30.
 XX
 PT Use of new and known peptide(s) for inhibition of polymerisation of
 PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
 PT Down's syndrome associated with amyloidosis.
 XX
 PS Example 1; Page 10; 31pp; English.
 XX
 CC This sequence represents a fragment of the amyloid beta peptide
 CC (residues 11-20). The invention relates to the use of peptide
 CC compounds for inhibition of polymerisation of amyloid beta peptide
 CC (ABP), as model substances for synthesis of ABP-ligands for inhibition
 CC of polymerisation of ABP, as a tool for the identification of other
 CC organic compounds with similar functional properties, or as ligands in
 CC positron emission tomography. The peptides may be used in treatment of
 CC amyloidosis, especially in treatment of Alzheimer's disease associated
 CC with amyloidosis, for treatment or prevention of dementia in patients with
 CC Down's syndrome, for treatment or prevention of hereditary cerebral
 CC haemorrhage with amyloidosis (Dutch type) or for the prevention of
 CC fibril formation of human amyloid protein. They can also be used for
 CC identifying other molecules with similar properties and/or as ligands
 CC for detection of amyloid deposits using e.g. positron emission
 CC tomography.
 CC
 SQ Sequence 10 AA;
 Query Match 83.6%; Score 46; DB 18; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0086;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHOKLVFF 8
 Db 3 HHOKLVFF 10
 RESULT 9
 AAB46223
 ID AAB46223 standard; peptide; 10 AA.
 XX
 AC AAB46223;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human APP derived immunogenic peptide #19.
 XX
 KM Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KM Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KM amyloid precursor protein; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200072880-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US1810.
 XX
 PR 28-MAY-1999; 99US-0322289.
 XX
 PA (NEUR-) NEURALAB LTD.
 XX
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX WPI; 2001-032104/04.
 DR
 XX Preventing or treating a disease associated with amyloid deposits,

PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX
 PS Disclosure; Figure 19; 143pp; English.
 XX
 CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
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 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 CC
 SQ Sequence 10 AA;
 Query Match 83.6%; Score 46; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0086;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHOKLVFF 8
 Db 3 HHOKLVFF 10
 RESULT 10
 AAM02310
 ID AAM02310 standard; peptide; 8 AA.
 XX
 AC AAM02310;
 XX
 DT 02-MAY-1997 (first entry)
 XX
 DE Beta-amyloid modulator peptide #1.
 XX
 KM Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
 KM cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
 KM familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
 KM isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
 KM bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
 KM adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
 KM scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 PN WO9628471-A1.
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 PD 19-SEP-1996.
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 PF 14-MAR-1996; 96WO-US03492.
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 PR 27-OCT-1995; 95US-0548998.
 PR 14-MAR-1995; 95US-0404831.
 PR 07-JUN-1995; 95US-0475579.
 XX
 PA (PHAR-) PHARM PEPTIDES INC.
 XX
 PI Benjamin H, Chin J, Findels MA, Garnick MB, Gefter ML;
 PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
 PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;
 XX WPI; 1996-433762/43.
 DR
 XX Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
 PT protein coupled (in)directly to at least 1 modifying gp., useful in
 PT treatment of Alzheimer's disease
 XX
 XX Claim 16; Page 90; 106pp; English.

XX AAW02310-W02332 represent the peptide portions of the beta-amyloid
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4
 CC kilodalton peptide that is the major protein component of amyloid
 CC plaques. Amyloid plaques are present both in the brain lesions, and in
 CC the walls of cerebral blood vessels in Alzheimer's disease patients.
 CC The amyloid modulators of the invention comprise an amyloidogenic protein
 CC or peptide (such as this sequence) coupled directly or indirectly to at
 CC least one modifying group. The modifying group is preferably a cyclic,
 CC heterocyclic, or polycyclic group, such as decalin, a cholanyl group, a
 CC biotin containing group, or a fluorescein containing group. These
 CC compounds then modulate the aggregation of these sequences to natural
 CC amyloid proteins or peptides when contacted with the natural
 CC amyloidogenic proteins or peptides. The modulator compounds can be used
 CC in the treatment of disorders associated with amyloidosis, such as
 CC familial amyloid polynuropathy, familial amyloid cardiomyopathy,
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
 CC and other types of amyloidosis. The modulators are also useful for the
 CC treatment of disorders associated with beta-amyloidosis, especially
 CC Alzheimer's disease.

XX Sequence 8 AA:

Query Match 76.4%; Score 42; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HQKLVEFA 9
 Db 1 HQKLVEFA 8

RESULT 11

AAW89374
 ID AAW89374 standard; peptide; 8 AA.

XX AAW89374:

XX 02-MAR-1999 (first entry)

XX Beta-amyloid peptide derivative A-beta-14-21.

XX Human: beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
 KM aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;

KM familial amyloid polynuropathy; bovine spongiform encephalopathy;
 KM Creutzfeldt-Jakob disease; bAP.

XX Homo sapiens.

OS Synthetic.

XX 05S854204-A.

XX 29-DEC-1998.

XX 14-MAR-1996; 96US-0612785.

XX 14-MAR-1996; 96US-0612785.

XX 14-MAR-1995; 95US-0404831.

XX 07-JUN-1995; 95US-0475579.

XX 27-OCT-1995; 95US-0548998.

XX (PRAE-) PRAECIS PHARM INC.

XX Benjamin H, Chin J, Flindels MA, Garnick MB, Gefter ML;

XX Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;

XX Molinaux S, Musso G, Reed M, Signer ER, Wakefield J;

XX WPI; 1999-094964/08.

XX New peptide(s) derived from beta-amyloid peptide that inhibit

PT amyloid aggregation - and neurotoxicity, specifically for treatment
 PT and prevention of Alzheimer's disease

XX Example 12; Column 64; 52pp; English.

XX The present invention describes beta-amyloid peptide (bAP) derivatives.
 CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
 CC peptides, specifically bAP, and their neurotoxicity, so are useful for
 CC treating and preventing any disease involving amyloidosis, specifically

CC Alzheimer's disease but also Down's syndrome, familial amyloid
 CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and

CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
 CC these diseases, in vitro or in vivo, by detecting binding of bAP to

CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
 CC even when bAP is present in molar excess. The present sequence

XX represents a bAP derivative.

XX Sequence 8 AA:

Query Match 76.4%; Score 42; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HQKLVEFA 9
 Db 1 HQKLVEFA 8

RESULT 12

AAW45941
 ID AAW45941 standard; peptide; 7 AA.

XX AAW45941:

XX 30-JUN-1998 (first entry)

XX Amyloid beta peptide fragment.

XX Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
 KM positron emission tomography; PET; Down's syndrome; amyloidosis.

XX Homo sapiens.

XX W09721728-A1.

XX 19-JUN-1997.

XX 09-DEC-1996; 96WO-SE01621.

XX 29-DEC-1995; 95US-0009386.

XX 12-DEC-1995; 95SE-0004467.

XX (KARO-) KAROLINSKA INNOVATIONS AB.

XX Naerland J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;

XX WPI; 1997-332723/30.

XX Use of new and known peptide(s) for inhibition of polymerisation of
 PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or

PT Down's syndrome associated with amyloidosis.

XX Example 1; Figure 2B; 31pp; English.

XX This sequence represents a fragment of the amyloid beta peptide. The
 CC invention relates to the use of peptide compounds for inhibition of

CC polymerisation of amyloid beta peptide (ABP), as model substances for
 CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a

CC tool for the identification of other organic compounds with similar
 CC functional properties, or as ligands in positron emission tomography.

CC The peptides may be used in treatment of amyloidosis, especially in
 CC treatment of Alzheimer's disease associated with amyloidosis, for

CC treatment or prevention of demens in patients with Down's syndrome, for

CC treatment or prevention of hereditary cerebral haemorrhage with
CC amyloidosis (Dutch type) or for the prevention of fibril formation of
CC human amyloid protein. They can also be used for identifying other
CC molecules with similar properties and/or as ligands for detection of
CC amyloid deposits using e.g. positron emission tomography.

XX Sequence 7 AA:

SO Query Match 72.7%; Score 40; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVF 7
1 HHOXKLVF 7

RESULT 13
AAW45938
ID AAW45938 standard; peptide: 8 AA.

XX AAW45938;

DT 30-JUN-1998 (first entry)

DE Amyloid beta peptide fragment.

KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KM positron emission tomography; PET; Down's syndrome; amyloidosis.

OS Homo sapiens.

PN MO9721728-A1.

PD 19-JUN-1997.

PF 09-DEC-1996; 96WO-SE01621.

PR 29-DEC-1995; 95US-0009386.

PR 12-DEC-1995; 95SE-0004467.

PA (KARO-) KAROLINSKA INNOVATIONS AB.

PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;

DR WPI; 1997-332723/30.

PT Use of new and known peptide(s) for inhibition of polymerisation of
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT Down's syndrome associated with amyloidosis.

PS Example 1; Figure 2B; 31pp; English.

CC This sequence represents a fragment of the amyloid beta peptide. The
CC invention relates to the use of peptide compounds for inhibition of
CC polymerisation of amyloid beta peptide (ABP), as model substances for
CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC tool for the identification of other organic compounds with similar
CC functional properties, or as ligands in positron emission tomography.
CC The peptides may be used in treatment of amyloidosis, especially in
CC treatment of Alzheimer's disease associated with amyloidosis, for
CC treatment or prevention of demens in patients with Down's syndrome, for
CC treatment or prevention of hereditary cerebral haemorrhage with
CC amyloidosis (Dutch type) or for the prevention of fibril formation of
CC human amyloid protein. They can also be used for identifying other
CC molecules with similar properties and/or as ligands for detection of
CC amyloid deposits using e.g. positron emission tomography.

XX Sequence 8 AA:

SO Query Match 72.7%; Score 40; DB 18; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVF 7
1 HHOXKLVF 8

RESULT 14
AAW45936

ID AAW45936 standard; peptide: 9 AA.

XX AAW45936;

DT 30-JUN-1998 (first entry)

DE Amyloid beta peptide fragment.

KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KM positron emission tomography; PET; Down's syndrome; amyloidosis.

OS Homo sapiens.

PN MO9721728-A1.

PD 19-JUN-1997.

PF 09-DEC-1996; 96WO-SE01621.

PR 29-DEC-1995; 95US-0009386.

PR 12-DEC-1995; 95SE-0004467.

PA (KARO-) KAROLINSKA INNOVATIONS AB.

PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;

DR WPI; 1997-332723/30.

PT Use of new and known peptide(s) for inhibition of polymerisation of
PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
PT Down's syndrome associated with amyloidosis.

PS Example 1; Figure 2B; 31pp; English.

CC This sequence represents a fragment of the amyloid beta peptide. The
CC invention relates to the use of peptide compounds for inhibition of
CC polymerisation of amyloid beta peptide (ABP), as model substances for
CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
CC tool for the identification of other organic compounds with similar
CC functional properties, or as ligands in positron emission tomography.
CC The peptides may be used in treatment of amyloidosis, especially in
CC treatment of Alzheimer's disease associated with amyloidosis, for
CC treatment or prevention of demens in patients with Down's syndrome, for
CC treatment or prevention of hereditary cerebral haemorrhage with
CC amyloidosis (Dutch type) or for the prevention of fibril formation of
CC human amyloid protein. They can also be used for identifying other
CC molecules with similar properties and/or as ligands for detection of
CC amyloid deposits using e.g. positron emission tomography.

XX Sequence 9 AA:

SO Query Match 72.7%; Score 40; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVF 7
3 HHOXKLVF 9

RESULT 15
AAB46222

ID AAB46222 standard; peptide: 10 AA.

XX AAB46222;

[illegible]

PD	07-DEC-2000.
XX	
PE	26-MAY-2000; 2000WO-US14810.
XX	
PR	28-MAY-1999; 99US-0322289.
XX	
PA	(NEUR-) NEURALAB LTD.
XX	
PI	Schenk DB, Bard F, Vasquez NJ, Yednock T;
DR	WPI: 2001-032104/04.
XX	
PT	Preventing or treating a disease associated with amyloid deposits,
PT	especially Alzheimer's disease, comprises administering amyloid
PT	specific antibody -
XX	
PS	Disclosure; Figure 19; 143pp; English.
XX	
CC	This invention describes a novel method of preventing or treating a
CC	disease associated with amyloid deposits of amyloid precursor protein
CC	(APP) Abeta fragments in the brain of a patient, which comprises
CC	administering to the patient: (a) an antibody that binds to Abeta, the
CC	antibody binds to an amyloid deposit and induces a clearing response (Fc
CC	receptor mediated phagocytosis) against it (b) a polypeptide containing
CC	an N-terminal segment of at least residues 1-3 of Abeta; or (c) an agent
CC	that induces an immunogenic response against residues 1-3 to 7-11 of
CC	Abeta. The products of the invention have neurotropic and neuroprotective
CC	activity. The method is also useful for monitoring a course of treatment
CC	being administered to a patient e.g. active and passive immunization. The
CC	methods are useful for prophylactic and therapeutic treatment of
CC	Alzheimer's disease.
XX	
SO	Sequence 10 AA:
Query Match	70.9%; Score 39; DB 22; Length 10;
Best Local Similarity	100.0%; Pred. No. 0.21;
Matches 8; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	3 OKLVFFAE 10
Dd	1 OKLVFFAE 8
RESULT 17	
AAR45231	
ID AAR45231 standard; Peptide: 7 AA.	
AC AAR45231;	
DT 20-JUN-1994 (first entry)	
DE Beta amyloid protein fragment.	
KW Amyloid precursor protein; APP; beta amyloid protein; BAP;	
KW detection; Alzheimer's disease; Down's syndrome.	
OS Homo sapiens.	
PN ADG338358-A.	
PD 04-NOV-1993.	
PE 03-MAY-1993; 93AU-0038358.	
PR 01-MAY-1992; 92US-0877675.	
PA (AMCY) AMERICAN CYANAMID CO.	
PI Jacobsen JS, Vittek MP;	
WI: 1993-406194/51.	
N-PSDB; AAO54259.	

XX New mutant forms of amyloid precursor protein - for detecting
 PT clds. that modify activity of enzymes involved in precursor
 PT cleavage, also new nucleic acid encoding them
 XX
 PS Disclosure; Page 34; 66pp; English.
 CC
 CC Recombinant polypeptides produced using the coding sequences of
 CC mutant forms of amyloid precursor proteins comprising from the 5' to
 CC the 3' end a sequence encoding a marker and either (1) a sequence
 CC encoding the N-terminus of an amyloid precursor protein (APP) up to,
 CC but not including, the nucleotides encoding the beta amyloid protein
 CC (BAP) domain or (2) the BAP domain; or the two ligated together, can
 CC be used to detect drugs or compounds that inhibit/augment the
 CC activity of proteolytic enzymes which cleave APP to generate BAP
 CC fragments (deposition of which occurs in patients with Alzheimers
 CC disease and Down's syndrome). This fragment corresponding to amino
 CC acid residues 14-20 of BAP can be altered and affect the level of
 CC secretion of APP's containing the BAP sequence.
 XX
 SQ Sequence 7 AA:
 Query Match 69.1%; Score 38; DB 14; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 HOKLVEF 8
 Db 1 HOKLVEF 7
 RESULT 18
 AAW02311
 ID AAW02311 standard; peptide: 7 AA.
 AC AAW02311;
 DT 02-MAY-1997 (first entry)
 XX
 DE Beta-amyloid modulator peptide #2.
 XX
 KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
 KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
 KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
 KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
 KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 PN WO9628471-A1.
 XX
 PD 19-SEP-1996.
 XX
 PF 14-MAR-1996; 96WO-US03492.
 XX
 PR 27-OCT-1995; 95US-0548998.
 PR 14-MAR-1995; 95US-0404831.
 PR 07-JUN-1995; 95US-0475579.
 XX
 PA (PHAR-) PHARM PEPTIDES INC.
 XX
 PI Benjamin H, Chin J, Findels MA, Garnick MB, Gefter ML;
 PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
 PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;
 XX
 DR WPI; 1996-433762/43.
 XX
 XX Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
 PT protein coupled (in)directly to at least 1 modifying gp., useful in
 PT treatment of Alzheimer's disease
 XX

PS Claim 16; Page 90; 106pp; English.
 XX
 CC AAW02310-W02332 represent the peptide portions of the beta-amyloid
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4
 CC kilodalton peptide that is the major protein component of amyloid
 CC plaques. Amyloid plaques are present both in the brain lesions, and in
 CC the walls of cerebral blood vessels in Alzheimer's disease patients.
 CC The amyloid modulators of the invention comprise an amyloidogenic protein
 CC or peptide (such as this sequence) coupled directly or indirectly to at
 CC least one modifying group. The modifying group is preferably a cyclic,
 CC heterocyclic, or polycyclic group, such as decalin, a cholanyl group, a
 CC biotin containing group, or a fluorescein containing group. These
 CC compounds then modulate the aggregation of these sequences to natural
 CC amyloid proteins or peptides when contacted with the natural
 CC amyloidogenic proteins or peptides. The modulator compounds can be used
 CC in the treatment of disorders associated with amyloidosis, such as
 CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
 CC and other types of amyloidosis. The modulators are also useful for the
 CC treatment of disorders associated with beta-amyloidosis, especially
 CC Alzheimer's disease.
 XX
 SQ Sequence 7 AA:
 Query Match 69.1%; Score 38; DB 17; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 HOKLVEF 8
 Db 1 HOKLVEF 7
 RESULT 19
 AAW45940
 ID AAW45940 standard; peptide: 7 AA.
 AC AAW45940;
 DT 30-JUN-1998 (first entry)
 XX
 DE Amyloid beta peptide fragment.
 XX
 KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
 KW positron emission tomography; PET; Down's syndrome; amyloidosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9721728-A1.
 XX
 PD 19-JUN-1997.
 XX
 PF 09-DEC-1996; 96WO-SE01621.
 XX
 PR 29-DEC-1995; 95US-0009386.
 PR 12-DEC-1995; 95SE-0004467.
 XX
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 XX
 PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
 PI WPI; 1997-332723/30.
 XX
 DR
 XX
 XX Use of new and known peptide(s) for inhibition of polymerisation of
 PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
 PT Down's syndrome associated with amyloidosis.
 XX
 PS Example 1; Figure 2B; 31pp; English.
 XX
 CC This sequence represents a fragment of the amyloid beta peptide. The

CC invention relates to the use of peptide compounds for inhibition of
 CC polymerisation of amyloid beta peptide (ABP), as model substances for
 CC synthesis of ABP-1 ligands for inhibition of polymerisation of ABP, as a
 CC tool for the identification of other organic compounds with similar
 CC functional properties, or as ligands in position emission tomography.
 CC The peptides may be used in treatment of amyloidosis, especially in
 CC treatment of Alzheimer's disease associated with amyloidosis, for
 CC treatment or prevention of demens in patients with Down's syndrome, for
 CC treatment or prevention of hereditary cerebral haemorrhage with
 CC amyloidosis (Dutch type) or for the prevention of fibril formation of
 CC human amyloid protein. They can also be used for identifying other of
 CC molecules with similar properties and/or as ligands for detection of
 CC amyloid deposits using e.g. positron emission tomography.
 CC XX

SO Sequence 7 AA;

Query Match 69.1%; Score 38; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVEF 8
 |||||
 DB 1 HOKLVEF 7

RESULT 20

AAW89375
 ID AAW89375 standard; peptide: 7 AA.

XX AAW89375;

DT 02-MAR-1999 (first entry)

XX Beta-amyloid peptide derivative A-beta-14-20.

XX Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
 KM aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
 KM familial amyloid polyneuropathy; bovine spongiform encephalopathy;
 KM Creutzfeldt-Jakob disease; bAP.

XX Homo sapiens.

OS Synthetic.

XX US5854204-A.

XX 29-DEC-1998.

PF 14-MAR-1996; 96US-0612785.

XX 14-MAR-1996; 96US-0612785.

PR 14-MAR-1996; 96US-0612785.

PR 07-JUN-1995; 95US-0404831.

PR 27-OCT-1995; 95US-0475579.

XX (PRAE-) PRAECTIS PHARM INC.

XX Benjamin H, Chin J, Findels MA, Garnick MB, Gelfer ML;

PI Hundel A, Kasman L, Kelley M, Kubasek W, Lee J;

PI Moineaux S, Musso G, Reed M, Signer ER, Wakefield J;

XX WPI. 1999-094964/08.

XX New peptide(s) derived from beta-amyloid peptide that inhibit

PT amyloid aggregation - and neurotoxicity, specifically for treatment

CC and prevention of Alzheimer's disease

XX Example 12; Column 64; 52pp; English.

XX The present invention describes beta-amyloid peptide (bAP) derivatives.

CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and

CC peptides, specifically bAP, and their neurotoxicity, so are useful for

CC treating and preventing any disease involving amyloidosis, specifically

CC Alzheimer's disease but also Down's syndrome, familial amyloid

CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and
 CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
 CC these diseases, in vitro or in vivo, by detecting binding of bAP to
 CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
 CC even when bAP is present in molar excess. The present sequence
 CC represents a bAP derivative.
 CC XX

SO Sequence 7 AA;

Query Match 69.1%; Score 38; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVEF 8
 |||||
 DB 1 HOKLVEF 7

RESULT 21

AA45239
 ID AA45239 standard; peptide: 9 AA.

XX AA45239;

DT 20-JUN-1994 (first entry)

XX Mutant amyloid precursor protein fragment.

XX Amyloid precursor protein; APP; beta amyloid protein; BAP;

XX detection; Alzheimer's disease; Down's syndrome.

XX Homo sapiens.

XX AU9338358-A.

XX 04-NOV-1993.

PF 03-MAY-1993; 93AU-0038358.

PR 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vitek MP;

XX WPI. 1993-406194/51.

XX N-PSDB; AA054267.

PS Disclosure; Page 35; 66pp; English.

XX Recombinant polypeptides produced using the coding sequences of

CC mutant forms of amyloid precursor proteins comprising from the 5' to

CC the 3' end a sequence encoding a marker and either (1) a sequence

CC encoding the N-terminus of an amyloid precursor protein (APP) up to,

CC but not including, the nucleotides encoding the beta amyloid protein

CC (BAP) domain or (2) the BAP domain; or the two ligated together, can

CC be used to detect drugs or compounds that inhibit/augment the

CC activity of proteolytic enzymes which cleave APP to generate BAP

CC fragments (deposition of which occurs in patients with Alzheimers

CC disease and Down's syndrome). This is a fragment of amyloid

CC precursor protein containing a mutation which is associated with

CC diseases involving BAP deposition.

XX Sequence 9 AA;

Query Match 65.5%; Score 36; DB 14; Length 9;

Best Local Similarity 87.5%; Pred. No. 6.4e+05;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 OKLVEFAE 10
 |||||
 DB 1 OKLVEFAQ 8

RESULT 22

AAW45946
 ID AAW45946 standard; peptide; 6 AA.

AC AAW45946;

DT 30-JUN-1998 (first entry)

DE Amyloid beta peptide fragment.

KM Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
 KW positron emission tomography; PET; Down's syndrome; amyloidosis.

OS Homo sapiens.

PN MO9721728-A1.

PD 19-JUN-1997.

PF 09-DEC-1996; 96WO-SE01621.

PR 29-DEC-1995; 95US-0009386.

PR 12-DEC-1995; 95SE-0004467.

PA (KARO-) KAROLINSKA INNOVATIONS AB.

PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;

DR WPI: 1997-332723/30.

PT Use of new and known peptide(s) for inhibition of polymerisation of
 amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
 Down's syndrome associated with amyloidosis.

PS Example 1; Figure 2B; 31pp; English.

CC This sequence represents a fragment of the amyloid beta peptide. The
 CC invention relates to the use of peptide compounds for inhibition of
 CC polymerisation of amyloid beta peptide (ABP), as model substances for
 CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
 CC tool for the identification of other organic compounds with similar
 CC functional properties, or as ligands in positron emission tomography.
 CC The peptides may be used in treatment of amyloidosis, especially in
 CC treatment of Alzheimer's disease associated with amyloidosis, for
 CC treatment or prevention of dementia in patients with Down's syndrome, for
 CC treatment or prevention of hereditary cerebral haemorrhage with
 CC amyloidosis (Dutch type) or for the prevention of fibril formation of
 CC human amyloid protein. They can also be used for identifying other
 CC molecules with similar properties and/or as ligands for detection of
 CC amyloid deposits using e.g. positron emission tomography.

SO Sequence 6 AA;

Query Match 61.8%; Score 34; DB 18; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLV 6
 |||||
 DB 1 HHOKLV 6

RESULT 23

AAAR45232
 ID AAR45232 standard; peptide; 7 AA.

AC AAR45232;

XX

DT 20-JUN-1994 (first entry)

DE Beta amyloid protein fragment.

KM Amyloid precursor protein; APP; beta amyloid protein; BAP;
 KW detection; Alzheimer's disease; Down's syndrome.

OS Homo sapiens.

PN AU9338358-A.

PD 04-NOV-1993.

PF 03-MAY-1993; 93AU-0038358.

PR 01-MAY-1992; 92US-0877675.

PA (AMCY) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vittek MP;

DR WPI: 1993-406194/51.

DR N-PSDB; AAQ54260.

PT New mutant forms of amyloid precursor protein - for detecting
 PT cpds. that modify activity of enzymes involved in precursor
 PT cleavage, also new nucleic acid encoding them

PS Disclosure; Page 34; 66pp; English.

CC Recombinant polypeptides produced using the coding sequences of
 CC mutant forms of amyloid precursor proteins comprising from the 5' to
 CC the 3' end a sequence encoding a marker and either (1) a sequence
 CC encoding the N-terminus of an amyloid precursor protein (APP) up to,
 CC but not including, the nucleotides encoding the beta amyloid protein
 CC (BAP) domain or (2) the BAP domain; or the two ligated together, can
 CC be used to detect drugs or compounds that inhibit/augment the
 CC activity of proteolytic enzymes which cleave APP to generate BAP
 CC fragments (deposition of which occurs in patients with Alzheimers
 CC disease and Down's syndrome). This fragment corresponding to amino
 CC acid residues 14-20 of BAP has been altered and APP's containing
 CC the altered BAP sequence show 0% secretion compared with those
 CC containing the wild type BAP sequence.

SO Sequence 7 AA;

Query Match 61.8%; Score 34; DB 14; Length 7;
 Best Local Similarity 85.7%; Pred. No. 6.4e+05;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HOKLVEF 8
 |||||
 DB 1 HOKLVEF 7

RESULT 24

AAAR87921
 ID AAR87921 standard; peptide; 7 AA.

AC AAR87921;

DT 01-MAR-1996 (first entry)

DE Test peptide used in study of antagonism of amyloid beta protein.

KM amnesia; amyloid beta; Alzheimer's disease.

OS Synthetic.

PN MO9508999-A1.

PD 06-APR-1995.

XX

PF 16-SEP-1994; 94WO-US10475.
 XX
 PR 29-SEP-1993; 93US-0127904.
 XX
 PA (CITY) CITY OF HOPE.
 XX
 PI Roberts E;
 XX
 DR WPI; 1995-147244/19.
 XX
 PT New peptide(s) which block binding of amyloid beta protein - used
 PT for antagonising the amnesic effects of amyloid beta protein,
 PT partic. in Alzheimer's disease
 XX
 PS Disclosure; Page 9; 27pp; English.
 XX
 CC The invention relates to three new peptides which block the amnesic
 CC effects of amyloid beta protein and which can be used to ameliorate
 CC amnesia and other neurotoxicity in Alzheimer's disease caused by
 CC deposition of this protein. The peptides themselves are not amnesic or
 CC memory-enhancing. The new peptides are described in AAR87912, AAR87913
 CC and AAR87914.
 CC The present sequence is an additional peptide tested in the process
 CC but found not to be active.
 CC
 SQ Sequence 7 AA;
 XX
 SO
 Query Match 61.8%; Score 34; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 KLVFFAE 10
 |||||
 DB 1 KLVFFAE 7
 |||||
 RESULT 25
 AAR88300
 ID AAR88300 standard; peptide; 7 AA.
 XX
 AC AAR88300;
 XX
 DT 23-FEB-1996 (first entry)
 XX
 DE Non-amnesic peptide Beta-A4 (16-22).
 XX
 KW Memory; enhancer; topographic model; amnesic peptide binding site;
 KW beta A4.
 XX
 OS Synthetic.
 OS
 PN WO9507093-A1.
 XX
 PD 16-MAR-1995.
 XX
 PF 08-SEP-1994; 94WO-US10083.
 XX
 PR 08-SEP-1993; 93US-0117927.
 XX
 PA (CITY) CITY OF HOPE.
 XX
 PI Roberts E;
 XX
 DR WPI; 1995-123235/16.
 XX
 PT Topographic model for amnesic peptide binding - used to design
 PT cpts. which enhance memory; and new peptide(s) so designed
 XX
 PS Disclosure; Page 28; 51pp; English.
 XX
 CC The peptide AAR88300 corresponds to residues 16-22 of beta-A4 was
 CC designed as a potential memory enhancing peptide but was found not
 CC to be amnesic. (Amnesic peptides are memory-enhancing at lower

CC concentrations than those at which they cause amnesia).
 XX
 SQ Sequence 7 AA;
 XX
 SO
 Query Match 61.8%; Score 34; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 KLVFFAE 10
 |||||
 DB 1 KLVFFAE 7
 |||||
 RESULT 26
 AAR80370
 ID AAR80370 standard; peptide; 7 AA.
 XX
 AC AAR80370;
 XX
 DT 19-APR-1996 (first entry)
 XX
 DE Protein polymeric adhesion substrate glutamine donor peptide #20.
 DE
 KW Pendant group; repeating unit; enzyme recognition site; sealant; fibrin;
 KW enzymatic cross-linking; biocompatible material; structural integrity;
 KW medical adhesive; wound closure; tissue repair; transglutaminase;
 KW protein polymer adhesive substrate.
 XX
 OS Synthetic.
 OS
 PN WO9523611-A1.
 XX
 PD 08-SEP-1995.
 XX
 PF 03-MAR-1995; 95WO-US02728.
 XX
 PR 03-MAR-1994; 94US-0205518.
 XX
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 XX
 PI Cappelletto J;
 XX
 DR WPI; 1995-320413/41.
 XX
 DE Protein polymers comprising repeating units and sequences - capable
 DE of enzyme-catalysed covalent bond formation useful as a
 PT biocompatible material for wound closure and tissue repair
 PT
 XX
 PS Example 9; Page 75; 138pp; English.
 PS
 CC The peptides AAR80351-70 are examples of glutamine donor peptides which
 CC can be used to generate protein polymeric adhesion substrate (PPAS)
 CC config. repeats of non-fibrin cross-linking donor peptide sequences (see
 CC AAR80345-50 for examples of PPAS proteins). The PPAS proteins can be
 CC used as substrates in enzymatic cross-linking reactions catalysed by a
 CC transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be
 CC used in biological systems where in situ formation of a biocompatible
 CC material with structural integrity is required e.g. as medical adhesives
 CC and sealants or for wound closure or tissue repair.
 CC
 SQ Sequence 7 AA;
 XX
 SO
 Query Match 61.8%; Score 34; DB 16; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHOKLV 6
 |||||
 DB 2 HHOKLV 7
 |||||
 RESULT 27
 AAW02312

ID AAM02312 standard; peptide; 7 AA.
 XX AAM02312;
 AC
 XX 02-MAY-1997 (first entry)
 XX
 DE Beta-amyloid modulator peptide #3.
 XX
 KM Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
 KM cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
 KM familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
 KM isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
 KM bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
 KM adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
 KM scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 PN W09628471-A1.
 XX
 PD 19-SEP-1996.
 XX
 PF 14-MAR-1996; 96WO-0503492.
 XX
 PR 27-OCT-1995; 95US-0548998.
 PR 14-MAR-1995; 95US-0404831.
 PR 07-JUN-1995; 95US-0475579.
 XX
 PA (PHAR-) PHARM PEPTIDES INC.
 XX
 PI Benjamin H, Chin J, Findels MA, Garrick MB, Gelfer ML;
 PI Hundel A, Kasman L, Kelley M, Kubasek W, Lee J;
 PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;
 DR WPI; 1996-433762/43.
 XX
 PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
 PT protein coupled (in)directly to at least 1 modifying gp.; useful in
 PT treatment of Alzheimer's disease
 XX
 PS Claim 16; Page 91; 106pp; English.
 XX
 CC AAM02310-W02332 represent the peptide portions of the beta-amyloid
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4
 CC kilodalton peptide that is the major protein component of amyloid
 CC plaques. Amyloid plaques are present both in the brain lesions, and in
 CC the walls of cerebral blood vessels in Alzheimer's disease patients.
 CC The amyloid modulators of the invention comprise an amyloidogenic protein
 CC or peptide (such as this sequence) coupled directly or indirectly to at
 CC least one modifying group. The modifying group is preferably a cyclic,
 CC heterocyclic, or polycyclic group, such as decalin, a cholanyl group, a
 CC biotin containing group, or a fluorescein containing group. These
 CC compounds then modulate the aggregation of these sequences to natural
 CC amyloid proteins or peptides when contacted with the natural
 CC amyloidogenic proteins or peptides. The modulator compounds can be used
 CC in the treatment of disorders associated with amyloidosis, such as
 CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
 CC and other types of amyloidosis. The modulators are also useful for the
 CC treatment of disorders associated with beta-amyloidosis, especially
 CC Alzheimer's disease.
 CC
 SQ Sequence 7 AA;
 XX

DB 1 OKLVEFA 7
 XX
 RESULT 28
 AAM45942
 ID AAM45942 standard; peptide; 7 AA.
 XX
 AC AAM45942;
 XX
 DE 30-JUN-1998 (first entry)
 XX
 KM Amyloid beta peptide fragment.
 KM Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
 KM position emission tomography; PET; Down's syndrome; amyloidosis.
 XX
 OS Homo sapiens.
 XX
 PN W09721728-A1.
 XX
 PD 19-JUN-1997.
 XX
 PF 09-DEC-1996; 96WO-SE01621.
 XX
 PR 29-DEC-1995; 95US-0009386.
 PR 12-DEC-1995; 95SE-0004467.
 XX
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 XX
 PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
 PI WPI; 1997-332723/30.
 XX
 PT Use of new and known peptide(s) for inhibition of polymerisation of
 PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
 PT Down's syndrome associated with amyloidosis.
 XX
 PS Example 1; Figure 2B; 31pp; English.
 XX
 CC This sequence represents a fragment of the amyloid beta peptide. The
 CC invention relates to the use of peptide compounds for inhibition of
 CC polymerisation of amyloid beta peptide (ABP), as model substances for
 CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
 CC tool for the identification of other organic compounds with similar
 CC functional properties, or as ligands in positron emission tomography.
 CC The peptides may be used in treatment of amyloidosis, especially in
 CC treatment of Alzheimer's disease associated with amyloidosis, for
 CC treatment or prevention of demens in patients with Down's syndrome, for
 CC treatment or prevention of hereditary cerebral haemorrhage with
 CC amyloidosis (Dutch type) or for the prevention of fibril formation of
 CC human amyloid protein. They can also be used for identifying other
 CC molecules with similar properties and/or as ligands for detection of
 CC amyloid deposits using e.g. positron emission tomography.
 CC
 SQ Sequence 7 AA;
 XX

Query Match 61.8%; Score 34; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHOKLV 6
 DB 2 HHOKLV 7
 XX

RESULT 29
 AAM49755
 ID AAM49755 standard; Peptide; 7 AA.
 XX
 AC AAM49755;
 XX
 DE 12-OCT-1998 (first entry)
 XX

DE Glutamine donor peptide.
 XX
 KM Protein polymer; adhesive sealant; wound healing; cross-linking.
 XX
 OS Synthetic.
 XX
 PN US5773577-A.
 XX
 PD 30-JUN-1998.
 XX
 PF 03-MAR-1994; 94US-0205518.
 XX
 PR 02-MAR-1995; 95US-0397633.
 PR 03-MAR-1994; 94US-0205518.
 XX
 PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 XX
 PI Cappello J;
 PI
 DR WPI; 1998-387091/33.
 XX
 PT New recombinant protein polymers - containing naturally occurring
 PT repetitive units for crosslinking by enzymes, useful as medical
 PT adhesives and sealants, depots and matrices
 PS
 PS Example 9; Column 49; 70pp; English.
 XX
 CC This is an example of a glutamine donor peptide that can be
 CC utilised in novel recombinant protein polymers of the invention.
 CC Such polymers (see AWW49710-28) typically comprise a repetitive
 CC amino acid backbone of repetitive units having a collagen, fibroin,
 CC elastin or keratin motif and at least 2 enzyme recognition
 CC sequences comprising a glutamine and/or lysine capable of enzyme
 CC catalysed isopeptide formation. The polymers are capable of
 CC covalent crosslinking by enzymatic reaction to form products which
 CC set quickly and have good adhesive properties and high strength.
 CC They can be used as medical adhesives and sealants, in the closure
 CC of wounds and repair of damaged tissues, prostheses coatings, drug
 CC depots, and matrices for the transplantation of cells.
 CC
 SO Sequence 7 AA;
 Query Match 61.8%; Score 34; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHOKLV 6
 DB 2 HHOKLV 7
 DB
 RESULT 30
 AAW89376
 ID AAW89376 standard; peptide; 7 AA.
 AC
 AC AAW89376;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 DE Beta-amyloid peptide derivative A-beta-15-21.
 XX
 KM Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
 KM aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
 KM familial amyloid polyneuropathy; bovine spongiform encephalopathy;
 KM Creutzfeldt-Jakob disease; bAP.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 PN US5854204-A.
 PD 29-DEC-1998.
 XX

PF 14-MAR-1996; 96US-0612785.
 XX
 PR 14-MAR-1996; 96US-0612785.
 PR 14-MAR-1995; 95US-0404831.
 PR 07-JUN-1995; 95US-0475579.
 PR 27-OCT-1995; 95US-0548998.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PI Benjamin H, Chin J, Flindels MA, Garnick MB, Geffer ML;
 PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
 PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
 XX
 DR WPI; 1999-094964/08.
 XX
 PT New peptide(s) derived from beta-amyloid peptide that inhibit
 PT amyloid aggregation - and neurotoxicity, specifically for treatment
 PT and prevention of Alzheimer's disease
 PS
 PS Example 12; Column 64; 52pp; English.
 XX
 CC The present invention describes beta-amyloid peptide (bAP) derivatives.
 CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
 CC peptides, specifically bAP, and their neurotoxicity, so are useful for
 CC treating and preventing any disease involving amyloidosis, specifically
 CC Alzheimer's disease but also Down's syndrome, familial amyloid
 CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and
 CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
 CC these diseases, in vitro or in vivo, by detecting binding of bAP to
 CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
 CC even when bAP is present in molar excess. The present sequence
 CC represents a bAP derivative.
 SO Sequence 7 AA;
 Query Match 61.8%; Score 34; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 OKLVFFA 9
 DB 1 OKLVFFA 7
 DB
 RESULT 31
 AAB67281
 ID AAB67281 standard; peptide; 7 AA.
 AC
 AC AAB67281;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE Residues 16-22 of Alzheimer's Abeta peptide.
 XX
 KM Alzheimer's; Abeta; beta-strand.
 XX
 OS Homo sapiens.
 XX
 PN WO200107473-A1.
 PD 01-FEB-2001.
 PF 28-JUL-2000; 2000MO-GH02901.
 PR 28-JUL-1999; 99GB-0017724.
 XX
 PA (STOR/) STORT K.
 XX
 PI Stort K;
 PI
 DR WPI; 2001-182777/18.
 XX
 PT Novel chemical compound or composition useful for preventing

PT beta-strand association, comprises peptides containing N-alpha
 substituted L-amino acids
 XX
 PS Claim 17; Page 46; 77pp; English.
 CC The present invention relates to a chemical compound or composition
 CC comprising a peptide with a beta strand forming section and
 CC associates with a target beta-strand formed by a separate
 CC peptide-containing molecule. The invention is useful for
 CC inhibiting or reversing the association of target beta-strand,
 CC formed by Alzheimer's Abeta peptide into a beta-sheet or beta-fibre
 CC and the aggregation of proteins or peptides.
 XX
 SQ Sequence 7 AA:
 Query Match 61.8%; Score 34; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 4 KLVFFAE 10
 |||||
 DB 1 KLVFFAE 7
 RESULT 32
 AAM45939
 ID AAM45939 standard; peptide; 8 AA.
 XX
 AC AAM45939;
 XX
 DT 30-JUN-1998 (first entry)
 XX
 DE Amyloid beta peptide fragment.
 XX
 KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
 KW positron emission tomography; PET; Down's syndrome; amyloidosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9721728-A1.
 PD 19-JUN-1997.
 XX
 PF 09-DEC-1996; 96MO-SE01621.
 XX
 PR 29-DEC-1995; 95US-0009386.
 PR 12-DEC-1995; 95SE-0004467.
 XX
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 XX
 PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
 XX WPI; 1997-332723/30.
 DR
 XX
 PT Use of new and known peptide(s) for inhibition of polymerisation of
 PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
 PT Down's syndrome associated with amyloidosis.
 XX
 PS Example 1; Figure 2B; 31pp; English.
 XX
 PS This sequence represents a fragment of the amyloid beta peptide. The
 CC invention relates to the use of peptide compounds for inhibition of
 CC polymerisation of amyloid beta peptide (ABP), as model substances for
 CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
 CC tool for the identification of other organic compounds with similar
 CC functional properties, or as ligands in positron emission tomography.
 CC The peptides may be used in treatment of amyloidosis, especially in
 CC treatment of Alzheimer's disease associated with amyloidosis, for
 CC treatment or prevention of demens in patients with Down's syndrome, for
 CC treatment or prevention of hereditary cerebral haemorrhage with
 CC amyloidosis (dutch type) or for the prevention of fibril formation of
 CC human amyloid protein. They can also be used for identifying other
 CC molecules with similar properties and/or as ligands for detection of

CC amyloid deposits using e.g. positron emission tomography.
 XX
 SQ Sequence 8 AA:
 Query Match 61.8%; Score 34; DB 18; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHQKLV 6
 |||||
 DB 3 HHQKLV 8
 RESULT 33
 AAM32551
 ID AAM32551 standard; peptide; 8 AA.
 XX
 AC AAM32551;
 XX
 DT 21-JAN-1998 (first entry)
 XX
 DE Amyloidogenic sequence amyloid beta-peptide.
 XX
 KW Anti-amyloid peptide; Abeta; abnormal protein folding inhibitor;
 KW Alzheimer's disease; dementia; Down's syndrome; amyloidosis disorder;
 KW human prion disease; Kuru; Creutzfeldt-Jakob disease;
 KW Gerstmann-Strausler-Scheinker Syndrome; animal prion disease;
 KW prion associated human neurodegenerative disease; scrapie;
 KW spongiform encephalopathy; transmissible mink encephalopathy;
 KW chronic wasting disease; mule; deer; elk; human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO9639834-A1.
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96MO-US10220.
 XX
 PR 10-APR-1996; 96US-0630645.
 PR 07-JUN-1995; 95US-0478326.
 XX
 PA (UYN) UNIV NEW YORK STATE.
 XX
 PI Baumann MH, Frangione B, Soto-Jara C;
 XX WPI; 1997-051637/05.
 DR
 XX
 PT New inhibitors of fibrillogenesis proteins or peptides - used for
 PT preventing, treating or detecting amyloidosis disorders such as
 PT Alzheimer's disease.
 XX
 PS Disclosure; Fig 1a; 63pp; English.
 XX
 PS A method has been developed for the prevention or treatment of a
 CC disorder or disease associated with the formation of amyloid or
 CC amyloid-like deposits, involving the abnormal folding of a protein
 CC or peptide. The method involves administering an inhibitory peptide
 CC which prevents the abnormal folding or which dissolves existing amyloid
 CC or amyloid-like deposits, where the peptide comprises a sequence of
 CC 3-15 amino acid residues and has a hydrophobic cluster of at least 3
 CC amino acids, where at least one of the 3 amino acids is a beta-sheet
 CC breaking amino acid residue selected from pro, gly, Asn and His. The
 CC present sequence represents an amyloidogenic sequence, amyloid beta-
 CC peptide, which is involved in the formation of several amyloid beta-
 CC The inhibitory peptide is capable of associating with a structural
 CC determinant on the protein or peptide to structurally block and inhibit
 CC the abnormal folding into amyloid or amyloid-like deposits. The method
 CC can be used for preventing, treating or detecting e.g. Alzheimer's
 CC dementia or disease, Down's syndrome, other amyloidosis disorders,
 CC human prion diseases such as Kuru, Creutzfeldt-Jakob disease, Gerstmann-
 CC Strausler-Scheinker Syndrome, prion associated human neurodegenerative

CC diseases or animal prion diseases such as scrapie, spongiform
CC encephalopathy, transmissible mink encephalopathy and chronic wasting
CC disease of mule deer and elk.
XX

SO Sequence 8 AA;

Query Match 61.8%; Score 34; DB 18; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLVFFAE 10
|||||
Db 1 KLVFFAE 7

RESULT 34

AAE10663
ID AAE10663 standard; peptide; 8 AA.

XX AAE10663;

XX 10-DEC-2001 (first entry)

DE Human amyloid precursor protein substrate alpha-secretase peptide #2.

XX Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;
KM Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
KM amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
KM alpha-secretase.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Cleavage-site 4..5

XX GB357767-A.

XX 04-JUL-2001.

XX 22-SEP-2000; 2000GB-0023315.

XX 23-SEP-1999; 99US-0155493.

XX 23-SEP-1999; 99US-0404133.

XX 13-SEP-1999; 99MO-US20881.

XX 06-DEC-1999; 99US-0416901.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Bienkowski MJ, Gurney M;

XX WPI; 2001-444208/48.

XX Polypeptide comprising fragments of human aspartyl protease with
XX amyloid precursor protein processing activity and alpha-secretase
XX activity, for identifying modulators useful in treating Alzheimer's
XX disease -

XX Claim 10; Page 163; 187pp; English.

XX The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC Asp1 proteins which lack transmembrane domain or amino terminal
CC domain or cytoplasmic domain and retains alpha-secretase activity
CC and amyloid protein precursor (APP) processing activity. The proteins
CC of the invention are useful for assaying hu-Asp1 alpha-secretase
CC activity, which in turn is useful for identifying modulators of
CC hu-Asp1 alpha-secretase activity, where modulators that increase
CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
CC disease (AD) which causes progressive dementia with consequent
CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
CC the substrate under acidic conditions and determining the level of

CC hu-Asp1 proteolytic activity. The present sequence is human amyloid
CC precursor protein (APP) substrate alpha-secretase peptide which is
CC used for determining the enzymatic activity of Asp-1 protein lacking
CC transmembrane domain (TM) and containing a (His)₆ tag.
XX

SO Sequence 8 AA;

Query Match 61.8%; Score 34; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLVFFAE 10
|||||
Db 1 KLVFFAE 7

RESULT 35

AAE02615
ID AAE02615 standard; peptide; 8 AA.

XX AAE02615;

XX 10-AUG-2001 (first entry)

DE Human amyloid precursor protein substrate alpha-secretase peptide #2.

XX Human; alpha-secretase; amyloid precursor protein; APP; therapy;
KM Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp1;
KM beta-secretase.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Cleavage-site 4..5

XX WO200123533-A2.

XX 05-APR-2001.

XX 22-SEP-2000; 2000MO-US26080.

XX 23-SEP-1999; 99US-0155493.

XX 23-SEP-1999; 99MO-US20881.

XX 13-OCT-1999; 99US-0416901.

XX 06-DEC-1999; 99US-0169232.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Gurney M, Bienkowski MJ;

XX WPI; 2001-290516/30.

XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
XX protein, useful for the treatment of Alzheimer's disease -

XX Claim 10; Page 98; 189pp; English.

XX The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying those enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human amyloid precursor
CC protein (APP) substrate alpha-secretase peptide which is used for
CC determining the enzymatic activity of Asp-1 deltatm (His)₆ protein.
XX

SO Sequence 8 AA;

Query Match 61.8%; Score 34; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLVFFAE 10

Db 1 KLVFFAE 7
|||||
RESULT 36
ID AAY7938
AAV79938 standard; peptide; 10 AA.
XX
AC AAV79938;
XX
DT 11-MAY-2000 (first entry)
XX
DE Beta-amyloid recognition peptide SEQ ID NO:3.
XX
KM Beta-amyloid; inhibitor; recognition element; hybrid; aggregation;
KM Alzheimer's disease; neuroprotective; nootropic.
XX
OS Homo sapiens.
XX
PN US6022859-A.
XX
PD 08-FEB-2000.
XX
PE 14-NOV-1997; 97US-0970833.
XX
PR 15-NOV-1996; 96US-0030840.
XX
PA (MISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Murphy RM, Klessling LT;
XX
DR WPI; 2000-160387/14.
XX
PT Beta-amyloid inhibitor useful for treating Alzheimer's disease -
XX
PS Example; Column 7; 15pp; English.
XX
CC The present invention describes a beta-amyloid inhibitor peptide.
CC Beta-amyloid inhibitors have neuroprotective and nootropic
CC properties. The inhibitor peptides are useful for the treatment of
CC Alzheimer's disease. The present sequence represents a beta-amyloid
CC recognition peptide used in the exemplification of present invention.
XX
SQ Sequence 10 AA;
Query Match 61.8%; Score 34; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 KLVFFAE 10
|||
Db 1 KLVFFAE 7
RESULT 37
ID AAB46221
AAB46221 standard; peptide; 10 AA.
XX
AC AAB46221;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #17.
XX
KM Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KM Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KM amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.

XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody.
XX
PS Disclosure; Figure 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
XX
SQ Sequence 10 AA;
Query Match 61.8%; Score 34; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHOKLV 6
|||||
Db 5 HHOKLV 10
RESULT 38
ID AAB46228
AAB46228 standard; peptide; 10 AA.
XX
AC AAB46228;
XX
DT 04-APR-2001 (first entry)
XX
DE Human APP derived immunogenic peptide #24.
XX
KM Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
KM Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
KM amyloid precursor protein; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200072880-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US14810.
XX
PR 28-MAY-1999; 99US-0322289.
XX
PA (NEUR-) NEURALAB LTD.
XX
PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
XX
DR WPI; 2001-032104/04.
XX
PT Preventing or treating a disease associated with amyloid deposits,

PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX
 XX
 PS Disclosure; Figure 19; 143pp; English.
 CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 CC
 XX
 SQ Sequence 10 AA;
 Query Match 61.8%; Score 34; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KLVFFAE 10
 |||||
 Db 1 KLVFFAE 7
 RESULT 39
 AAM45945
 ID AAM45945 standard; peptide; 6 AA.
 XX
 AC AAM45945;
 XX
 DT 30-JUN-1998 (first entry)
 XX
 DE Amyloid beta peptide fragment.
 XX
 KM Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
 KM positron emission tomography; PET; Down's syndrome; amyloidosis.
 XX
 OS Homo sapiens.
 OS
 PN MO9721728-A1.
 XX
 PD 19-JUN-1997.
 XX
 PF 09-DEC-1996; 96WO-S01621.
 XX
 PR 29-DEC-1995; 95US-0009386.
 PR 12-DEC-1995; 95SE-0004467.
 XX
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 XX
 PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
 XX
 DR WPI; 1997-332723/30.
 XX
 PT Use of new and known peptide(s) for inhibition of polymerisation of
 PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
 PT Down's syndrome associated with amyloidosis.
 XX
 PS Example 1; Figure 2B; 31pp; English.
 CC This sequence represents a fragment of the amyloid beta peptide. The
 CC invention relates to the use of peptide compounds for inhibition of
 CC polymerisation of amyloid beta peptide (ABP), as model substances of
 CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
 CC tool for the identification of other organic compounds with similar
 CC functional properties, or as ligands in positron emission tomography.
 CC The peptides may be used in treatment of amyloidosis, especially in

CC treatment of Alzheimer's disease associated with amyloidosis, for
 CC treatment or prevention of demens in patients with Down's syndrome, for
 CC treatment or prevention of hereditary cerebral hemorrhage with
 CC amyloidosis (Dutch type) or for the prevention of fibril formation of
 CC human amyloid protein. They can also be used for identifying other
 CC molecules with similar properties and/or as ligands for detection of
 CC amyloid deposits using e.g. positron emission tomography.
 CC
 XX
 SQ Sequence 6 AA;
 Query Match 58.2%; Score 32; DB 18; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HOKLVF 7
 |||||
 Db 1 HOKLVF 6
 RESULT 40
 AAR45233
 ID AAR45233 standard; Peptide; 7 AA.
 XX
 AC AAR45233;
 XX
 DT 20-JUN-1994 (first entry)
 XX
 DE Beta amyloid protein fragment.
 XX
 KM Amyloid precursor protein; APP; beta amyloid protein; BAP;
 KM detection; Alzheimer's disease; Down's syndrome.
 XX
 OS Homo sapiens.
 OS
 PN AU9338358-A.
 XX
 PD 04-NOV-1993.
 XX
 PF 03-MAY-1993; 93AU-0038358.
 XX
 PR 01-MAY-1992; 92US-087675.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vittek MP;
 XX
 DR WPI; 1993-406194/51.
 DR N-PSDB; AAO54261.
 XX
 PT New mutant forms of amyloid precursor protein - for detecting
 PT cpds. that modify activity of enzymes involved in precursor
 PT cleavage, also new nucleic acid encoding them
 XX
 PS Disclosure; Page 34; 66pp; English.
 CC Recombinant polypeptides produced using the coding sequences of
 CC mutant forms of amyloid precursor proteins comprising from the 5' to
 CC the 3' end a sequence encoding a marker and either (1) a sequence
 CC encoding the N-terminus of an amyloid precursor protein (APP) up to,
 CC but not including, the nucleotides encoding the beta amyloid protein
 CC (BAP) domain or (2) the BAP domain; or the two ligated together, can
 CC be used to detect drugs or compounds that inhibit/augment the
 CC activity of proteolytic enzymes which cleave APP to generate BAP
 CC fragments (deposition of which occurs in patients with Alzheimers
 CC disease and Down's syndrome). This fragment corresponding to amino
 CC acid residues 14-20 of BAP has been altered and APP's containing
 CC the altered BAP sequence show 10-20% secretion compared with those
 CC containing the wild type BAP sequence.
 CC
 XX
 SQ Sequence 7 AA;
 Query Match 56.4%; Score 31; DB 14; Length 7;
 Best Local Similarity 85.7%; Pred. No. 6.4e+05;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 HOKLVEF 8
 |||||
 Db 1 HOKLVEF 7

RESULT 41
 AAB82639
 ID AAB82639 standard; Peptide: 7 AA.
 XX
 AC AAB82639;
 XX
 DT 02-OCT-2001 (first entry)
 XX
 DE All-D peptide used in Alzheimer's disease vaccine.
 XX
 KM Alzheimer's disease; amyloidosis; amyloid-related disease;
 KW vaccine; therapy; antigen.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..7
 /note= "all D-form residues"
 XX
 PN WO200139796-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 29-NOV-2000; 2000WO-CA01413.
 XX
 PR 29-NOV-1999; 99US-0168594.
 PR 28-NOV-2000; 2000US-0724842.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Chalfour R, Hebert L, Kong X, Gervais F;
 XX
 DR WPI; 2001-441458/47.
 XX
 PT Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, e.g. as
 PT vaccine, which elicits production of antibodies to prevent
 PT fibrillogenesis and associated cellular toxicity -
 XX
 PA Disclosure; Page 11; 31pp; English.
 XX
 PS The present sequence is that of an all-D peptide suitable for
 CC use in preparing vaccines for preventing or treating Alzheimer's
 CC disease and other amyloid related disorders in humans. It is based
 CC on a portion of amyloid-beta peptide (see AAB82622), and may be
 CC modified by removing or inserting 1 or more amino acid residues, or
 CC by substituting 1 or more amino acid residues with other amino acid
 CC residues or non-amino acid fragments. Vaccines of the invention
 CC are produced using 'non-self' peptides synthesised from the
 CC unnatural D-configuration amino acids to avoid the drawbacks of
 CC 'self' proteins. The all-D peptides need not be aggregated to be
 CC operative or immunogenic. They preferably interact with at
 CC least 1 region of an amyloid protein, e.g. the beta-sheet region
 CC or GAG-binding site region, the amyloid-beta peptide, or their
 CC immunogenic fragments, protein conjugates, immunogenic derivative
 CC peptides and immunogenic peptidomimetics. Examples include all-D
 CC peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,
 CC 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D
 CC derivative peptides given in AAB82623-64. The vaccine elicits a
 CC preferential TH-2 or TH-1 response, preventing fibrillogenesis and
 CC associated cellular toxicity. The amyloid related diseases may be
 CC localised amyloidosis, e.g. diabetes type II, neurodegenerative
 CC diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob
 CC disease, scrapie, cerebral amyloid angiopathy, and prion protein
 CC related disorders, or systemic amyloidosis associated with chronic
 CC infection (e.g. tuberculosis) or chronic inflammation (e.g.

CC rheumatoid arthritis), familial Mediterranean fever (FMF) and
 CC systemic amyloidosis found in long-term haemodialysis patients.
 CC
 SQ Sequence 7 AA;
 Query Match 56.4%; Score 31; DB 22; Length 7;
 Best Local Similarity 85.7%; Pred. No. 6.4e+05;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 4 KLVFPAE 10
 |||||
 Db 1 KLVFPAE 7

RESULT 42
 AAB82640
 ID AAB82640 standard; Peptide: 7 AA.
 XX
 AC AAB82640;
 XX
 DT 02-OCT-2001 (first entry)
 XX
 DE All-D peptide used in Alzheimer's disease vaccine.
 XX
 KM Alzheimer's disease; amyloidosis; amyloid-related disease;
 KW vaccine; therapy; antigen.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..7
 /note= "all D-form residues"
 FT Modified-site 6
 /note= "C-terminal amide"
 XX
 PN WO200139796-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 29-NOV-2000; 2000WO-CA01413.
 XX
 PR 29-NOV-1999; 99US-0168594.
 PR 28-NOV-2000; 2000US-0724842.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Chalfour R, Hebert L, Kong X, Gervais F;
 XX
 DR WPI; 2001-441458/47.
 XX
 PT Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, e.g. as
 PT vaccine, which elicits production of antibodies to prevent
 PT fibrillogenesis and associated cellular toxicity -
 XX
 PA Disclosure; Page 11; 31pp; English.
 XX
 PS The present sequence is that of an all-D peptide suitable for
 CC use in preparing vaccines for preventing or treating Alzheimer's
 CC disease and other amyloid related disorders in humans. It is based
 CC on a portion of amyloid-beta peptide (see AAB82622), and may be
 CC modified by removing or inserting 1 or more amino acid residues, or
 CC by substituting 1 or more amino acid residues with other amino acid
 CC residues or non-amino acid fragments. Vaccines of the invention
 CC are produced using 'non-self' peptides synthesised from the
 CC unnatural D-configuration amino acids to avoid the drawbacks of
 CC 'self' proteins. The all-D peptides need not be aggregated to be
 CC operative or immunogenic. They preferably interact with at
 CC least 1 region of an amyloid protein, e.g. the beta-sheet region
 CC or GAG-binding site region, the amyloid-beta peptide, or their
 CC immunogenic fragments, protein conjugates, immunogenic derivative
 CC peptides and immunogenic peptidomimetics. Examples include all-D
 CC peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,

CC 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D
 CC derivative peptides given in AAB82623-64. The vaccine elicits a
 CC preferential TH-2 or TH-1 response, preventing fibrillogenesis and
 CC associated cellular toxicity. The amyloid related diseases may be
 CC localised amyloidosis, e.g. diabetes type II, neurodegenerative
 CC diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob
 CC disease, scrapie, cerebral amyloid angiopathy, and prion protein
 CC related disorders, or systemic amyloidosis associated with chronic
 CC infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and
 CC systemic amyloidosis found in long-term haemodialysis patients.
 CC
 SQ Sequence 7 AA;

Query Match 56.4%; Score 31; DB 22; Length 7;
 Best Local Similarity 85.7%; Pred. No. 6.4e+05;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KLVFFAE 10
 |||||:
 Db 1 KLVFFAQ 7

RESULT 43
 ID AAB48491 standard; Peptide: 7 AA.
 XX

AC AAB48491;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Antifibrillogenic peptide #18.
 XX

KW Neotropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX

OS Homo sapiens.
 XX

PN WO200068263-A2.
 XX

PD 16-NOV-2000.
 XX

PF 04-MAY-2000; 2000MO-CA00515.
 XX

PR 05-MAY-1999; 99US-0132592.
 XX

PA (NEUR-) NEUROCHEM INC.
 XX

PI Chalfour R, Gervais F, Gupta A;
 XX

DR WPI: 2001-031852/04.
 XX

PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic -
 XX

PS Claim 7; Page 25; 46pp; English.
 XX

CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are
 CC therefore useful for treating amyloidosis disorders such as Alzheimer's
 CC disease. Peptides AAB48474-B48496 were identified from the
 CC glycosaminoglycan binding region and the prot-prot interaction region of
 CC the human amyloid protein.
 CC
 SQ Sequence 7 AA;

Query Match 56.4%; Score 31; DB 22; Length 7;
 Best Local Similarity 85.7%; Pred. No. 6.4e+05;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFFAE 10
 |||||:
 Db 1 KLVFFAQ 7

RESULT 44
 ID AAB48492 standard; Peptide: 7 AA.
 XX

AC AAB48492;
 XX
 DT 02-MAR-2001 (first entry)
 XX

DE Antifibrillogenic peptide #19.
 XX

KW Neotropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX

OS Homo sapiens.
 XX

PN Key Location/Qualifiers
 FT Modified-site 7
 FT /note="C-terminal amide"
 XX

PN WO200068263-A2.
 XX

PD 16-NOV-2000.
 XX

PF 04-MAY-2000; 2000MO-CA00515.
 XX

PR 05-MAY-1999; 99US-0132592.
 XX

PA (NEUR-) NEUROCHEM INC.
 XX

PI Chalfour R, Gervais F, Gupta A;
 XX

DR WPI: 2001-031852/04.
 XX

PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic -
 XX

PS Claim 7; Page 25; 46pp; English.
 XX

CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are
 CC therefore useful for treating amyloidosis disorders such as Alzheimer's
 CC disease. Peptides AAB48474-B48496 were identified from the
 CC glycosaminoglycan binding region and the prot-prot interaction region of
 CC the human amyloid protein.
 CC
 SQ Sequence 7 AA;

Query Match 56.4%; Score 31; DB 22; Length 7;
 Best Local Similarity 85.7%; Pred. No. 6.4e+05;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFFAE 10
 |||||:
 Db 1 KLVFFAQ 7

RESULT 45
 ID AAM45952 standard; peptide: 5 AA.
 XX

AC AAM45952;
 XX

DT 30-JUN-1998 (first entry)
 XX

DE Amyloid beta peptide fragment.

XX Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
 KM positron emission tomography; PET; Down's syndrome; amyloidosis.
 XX Homo sapiens.
 OS
 XX WO9721728-A1.
 PN
 XX 19-JUN-1997.
 PD
 XX 09-DEC-1996; 96WO-SE01621.
 PF
 XX 29-DEC-1995; 95US-0009386.
 PR
 XX 12-DEC-1995; 95SE-0004467.
 PA
 XX (KARO-) KAROLINSKA INNOVATIONS AB.
 PI
 XX Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
 DR WPI: 1997-332723/30.
 PT Use of new and known peptide(s) for inhibition of polymerisation of
 PT amyloid beta peptide e.g. for treatment of Alzheimer's disease or
 PT Down's syndrome associated with amyloidosis.
 PS
 XX Example 1; Figure 2b; 31pp; English.
 PS
 XX This sequence represents a fragment of the amyloid beta peptide. The
 CC invention relates to the use of peptide compounds for inhibition of
 CC polymerisation of amyloid beta peptide (ABP), as model substances for
 CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
 CC tool for the identification of other organic compounds with similar
 CC functional properties, or as ligands in positron emission tomography.
 CC The peptides may be used in treatment of amyloidosis, especially in
 CC treatment of Alzheimer's disease associated with amyloidosis, for
 CC treatment or prevention of hemiparesis in patients with Down's syndrome, for
 CC treatment or prevention of hereditary cerebral haemorrhage with
 CC amyloidosis (Dutch type) or for the prevention of fibril formation of
 CC human amyloid protein. They can also be used for identifying other
 CC molecules with similar properties and/or as ligands for detection of
 CC amyloid deposits using e.g. positron emission tomography.
 XX
 SQ Sequence 5 AA;
 QY
 OY 1 HHQRL 5
 DB 1 HHQRL 5
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query Match 54.5%; Score 30; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 RESULT 46
 AAM02313
 ID AAM02313 standard; peptide; 6 AA.
 XX
 AC AAM02313;
 XX
 DT 02-MAY-1997 (first entry)
 XX
 DE Beta-amyloid modulator peptide #4.
 XX
 KM Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
 KM cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
 KM familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
 KM isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
 KM bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
 KM adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
 KM scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX

PN WO9628471-A1.
 XX
 PD 19-SEP-1996.
 XX
 PF 14-MAR-1996; 96WO-US03492.
 XX
 PR 27-OCT-1995; 95US-054898.
 PR 14-MAR-1995; 95US-0404831.
 PR 07-JUN-1995; 95US-0475579.
 XX
 XX (PHAR-) PHARM PEPTIDES INC.
 XX
 PI Benjamin H, Chin J, Finkelstein MA, Garnick MB, Geffer ML;
 PI Hundal A, Kasman L, Kelley M, Kudasek W, Lee J;
 PI Molineaux S, Musso G, Reed MJ, Signer ER, Wakefield J;
 DR WPI: 1996-433762/43.
 XX
 PT Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
 PT protein coupled (in)directly to at least 1 modifying gp., useful in
 PT treatment of Alzheimer's disease
 PS
 XX Claim 16; Page 91; 106pp; English.
 CC AAM02310-WO2332 represent the peptide portions of the beta-amyloid
 CC modulator compounds of the invention. Beta-amyloid peptide is a 4
 CC kilodalton peptide that is the major protein component of amyloid
 CC plaques. Amyloid plaques are present both in the brain lesions, and in
 CC the walls of cerebral blood vessels in Alzheimer's disease patients.
 CC The amyloid modulators of the invention comprise an amyloidogenic protein
 CC or peptide (such as this sequence) coupled directly or indirectly to at
 CC least one modifying group. The modifying group is preferably a cyclic,
 CC heterocyclic, or polycyclic group, such as decalin, a cholanlyl group, a
 CC biotin containing group, or a fluorescein containing group. These
 CC compounds then modulate the aggregation of these sequences to natural
 CC amyloid proteins or peptides when contacted with the natural
 CC amyloidogenic proteins or peptides. The modulator compounds can be used
 CC in the treatment of disorders associated with amyloidosis, such as
 CC familial amyloid polyneuropathy, familial amyloid cardiomyopathy,
 CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
 CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
 CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
 CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
 CC and other types of amyloidosis. The modulators are also useful for the
 CC treatment of disorders associated with beta-amyloidosis, especially
 CC Alzheimer's disease.
 XX
 SQ Sequence 6 AA;
 QY
 OY 3 OKLYVF 8
 DB 1 OKLYVF 6
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Query Match 54.5%; Score 30; DB 17; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 RESULT 47
 AAM45947
 ID AAM45947 standard; peptide; 6 AA.
 XX
 AC AAM45947;
 XX
 DT 30-JUN-1998 (first entry)
 XX
 DE Amyloid beta peptide fragment.
 XX
 KM Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
 KM positron emission tomography; PET; Down's syndrome; amyloidosis.
 XX
 OS Homo sapiens.
 XX

PN W09721728-A1.
 XX
 PD 19-JUN-1997.
 XX
 PE 09-DEC-1996; 96WO-SE01621.
 XX
 PR 29-DEC-1995; 95US-0009386.
 PR 12-DEC-1995; 95SE-0004467.
 XX
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 XX
 PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
 DR WPI: 1997-332723/30.
 XX
 PT Use of new and known peptide(s) for inhibition of polymerisation of
 PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
 PT Down's syndrome associated with amyloidosis.
 XX
 PS Example 1; Figure 2b; 31pp; English.
 XX
 CC This sequence represents a fragment of the amyloid beta peptide. The
 CC invention relates to the use of peptide compounds for inhibition of
 CC polymerisation of amyloid beta peptide (ABP), as model substances for
 CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
 CC tool for the identification of other organic compounds with similar
 CC functional properties, or as ligands in positron emission tomography.
 CC The peptides may be used in treatment of amyloidosis, especially in
 CC treatment of Alzheimer's disease associated with amyloidosis, for
 CC treatment or prevention of dementia in patients with Down's syndrome, for
 CC treatment or prevention of hereditary cerebral haemorrhage with
 CC amyloidosis (Dutch type) or for the prevention of fibril formation of
 CC human amyloid protein. They can also be used for identifying other
 CC molecules with similar properties and/or as ligands for detection of
 CC amyloid deposits using e.g. positron emission tomography.
 CC
 SQ Sequence 6 AA;
 Query Match 54.5%; Score 30; DB 18; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HQOKL 5
 DB 2 HQOKL 6
 RESULT 48
 AAW45944
 ID AAW45944 standard; peptide; 6 AA.
 XX
 AC AAW45944;
 XX
 DT 30-JUN-1998 (first entry)
 XX
 DE Amyloid beta peptide fragment.
 XX
 KW Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
 KW positron emission tomography; PET; Down's syndrome; amyloidosis.
 XX
 OS Homo sapiens.
 XX
 PN W09721728-A1.
 XX
 PD 19-JUN-1997.
 XX
 PE 09-DEC-1996; 96WO-SE01621.
 XX
 PR 29-DEC-1995; 95US-0009386.
 PR 12-DEC-1995; 95SE-0004467.
 XX
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 XX

PI Naslund J, Nordstedt C, Terenius L, Thyberg J, Tjernberg LO;
 XX
 DR WPI: 1997-332723/30.
 XX
 PT Use of new and known peptide(s) for inhibition of polymerisation of
 PT amyloid beta peptide - e.g. for treatment of Alzheimer's disease or
 PT Down's syndrome associated with amyloidosis.
 XX
 PS Example 1; Figure 2b; 31pp; English.
 XX
 CC This sequence represents a fragment of the amyloid beta peptide. The
 CC invention relates to the use of peptide compounds for inhibition of
 CC polymerisation of amyloid beta peptide (ABP), as model substances for
 CC synthesis of ABP-ligands for inhibition of polymerisation of ABP, as a
 CC tool for the identification of other organic compounds with similar
 CC functional properties, or as ligands in positron emission tomography.
 CC The peptides may be used in treatment of amyloidosis, especially in
 CC treatment of Alzheimer's disease associated with amyloidosis, for
 CC treatment or prevention of dementia in patients with Down's syndrome, for
 CC treatment or prevention of hereditary cerebral haemorrhage with
 CC amyloidosis (Dutch type) or for the prevention of fibril formation of
 CC human amyloid protein. They can also be used for identifying other
 CC molecules with similar properties and/or as ligands for detection of
 CC amyloid deposits using e.g. positron emission tomography.
 CC
 SQ Sequence 6 AA;
 Query Match 54.5%; Score 30; DB 18; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 OKLVFF 8
 DB 1 OKLVFF 6
 RESULT 49
 AAY39801
 ID AAY39801 standard; peptide; 6 AA.
 XX
 AC AAY39801;
 XX
 DT 29-NOV-1999 (first entry)
 XX
 DE Beta-amyloid protein fragment.
 XX
 KW Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling;
 KW long-standing inflammation; malignancy; Familial Mediterranean Fever;
 KW multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; kuru;
 KW carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;
 KW endocrine tumour; medullary carcinoma; Down's syndrome; scrapie;
 KW Creutzfeldt-Jakob disease; Gerstmann Strausler Syndrome;
 KW subacute spongiform encephalopathy; therapy.
 XX
 OS Homo sapiens.
 XX
 PN US5958883-A.
 XX
 PD 28-SEP-1999.
 XX
 PE 05-JUN-1995; 95US-0461216.
 XX
 PR 23-OCT-1992; 92US-0969734.
 PR 23-SEP-1992; 92US-0950417.
 XX
 PA (DNIM) UNIV WASHINGTON.
 XX
 PI Snow AD;
 XX
 DR WPI: 1999-561062/47.
 XX
 PT Peptides of 6-8 amino acids useful for treating or preventing
 PT amyloidosis -

XX Claim 1; Column 71; 83pp; English.
 XX
 CC This sequence represents a fragment of the beta-amyloid protein. The
 CC invention relates to a method for treating or preventing a form of
 CC amyloidosis, including Alzheimer's disease using this sequence. The
 CC compositions may be useful for treating or preventing the amyloidosis
 CC associated with long-standing inflammation, various forms of malignancy
 CC (including B-cell type malignancies), Familial Mediterranean Fever,
 CC multiple myeloma, plasma cell dyscrasias, long-term haemodialysis, carpal
 CC tunnel syndrome, joint swelling, multiple spontaneous fractures,
 CC radiolucency in the wrist and hip, endocrine tumours, medullary carcinoma
 CC of the thyroid, diabetes, Alzheimer's disease, Down's syndrome,
 CC Creutzfeldt-Jakob disease, Gerstmann Strausler Syndrome, kuru, scrapie
 CC and other subacute spongiform encephalopathies.
 CC
 SO Sequence 6 AA;
 Query Match 54.5%; Score 30; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HQKTL 5
 | | | | |
 DB 2 HQKTL 6
 RESULT 50
 AAW29090
 ID AAW29090 standard; peptide; 6 AA.
 AC AAW29090;
 XX
 DT 20-JUL-1999 (first entry)
 DE A-beta-binding peptide fragment conjugated to cyclosporin.
 XX
 KW Cyclosporin: A-beta peptide; conjugate; neurological disease;
 KW Alzheimer; multiple sclerosis; amyotrophic lateral sclerosis;
 KW ALS; non-immunosuppressive; amyloid plaque formation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6
 FT /note="The C-terminal is condensed onto the side
 FT chain of Lys(7) of the cyclosporin analog described
 FT in AAW29087, AAW29088, AAW29095 and AAW29097."
 PN WO9910374-A1.
 XX
 PD 04-MAR-1999.
 XX
 PF 25-AUG-1998; 98WO-US17544.
 XX
 PR 26-AUG-1997; 97US-0057751.
 XX
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Rich DH, Solomon ME;
 XX
 DR WPI; 1999-276928/23.
 XX
 PT New A-beta-binding peptide conjugates and Csa analogs - useful in
 PT treatment of neurological diseases e.g. Alzheimer's disease,
 PT multiple sclerosis etc.
 XX
 PS Claim 5; Page 98; 129pp; English.
 CC
 CC New conjugates are disclosed which are of formula A-Z, in which: A is
 CC (1) a cyclosporin A analogue described in AAW29087 or (2) an FK506
 CC binding peptide inhibitor; and Z is a polypeptide comprising 5 or more
 CC contiguous residues of A-beta peptide. The compounds are novel chemical

CC Inducers of dimerization which are non-immunosuppressive and which are
 CC inhibitors of A-beta peptide aggregation and deposition in amyloid
 CC plaques. The adverse consequences of amyloid plaque formation can be
 CC prevented or ameliorated by sequestering the A-beta peptide in monomeric
 CC form with a conjugate which links the A-beta to cyclophilin or FKBP,
 CC therefore providing a mechanism to minimize the amount of free A-beta
 CC available for fibril formation and deposition. The compounds can be used
 CC for the treatment of Alzheimer's disease, multiple sclerosis and
 CC amyotrophic lateral sclerosis.
 CC
 SO Sequence 6 AA;
 Query Match 54.5%; Score 30; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 OKLVFF 8
 | | | | |
 DB 1 OKLVFF 6

Search completed: October 29, 2002, 09:37:39
 Job time : 31 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 09:23:27 ; Search time 13 Seconds

(without alignments)
18.789 Million cell updates/sec

Title: US-09-724-842A-27

Sequence: 1 HHOKLVFAE 10

Scoring table: BIOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCrus.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	55	100.0	15	2 US-08-612-785B-37	Sequence 37, Appl
2	55	100.0	17	4 US-09-264-709A-2	Sequence 2, Appl
3	55	100.0	26	1 US-08-304-585-7	Sequence 7, Appl
4	55	100.0	28	1 US-08-346-849-4	Sequence 4, Appl
5	55	100.0	28	1 US-08-302-808-7	Sequence 7, Appl
6	55	100.0	28	2 US-08-609-090-2	Sequence 2, Appl
7	55	100.0	28	2 US-08-986-948-7	Sequence 7, Appl
8	55	100.0	28	2 US-08-293-284A-4	Sequence 4, Appl
9	55	100.0	28	2 US-08-461-216-2	Sequence 2, Appl
10	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
11	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
12	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
13	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
14	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
15	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
16	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
17	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
18	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
19	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
20	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
21	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
22	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
23	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
24	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
25	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
26	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl
27	55	100.0	28	4 US-09-388-890-3	Sequence 3, Appl

ALIGNMENTS

28	55	100.0	38	1 US-08-302-808-1	Sequence 1, Appl
29	55	100.0	38	2 US-07-737-371E-68	Sequence 68, Appl
30	55	100.0	38	2 US-08-986-948-1	Sequence 1, Appl
31	55	100.0	39	1 US-08-304-585-5	Sequence 5, Appl
32	55	100.0	39	1 US-08-302-808-2	Sequence 2, Appl
33	55	100.0	39	2 US-08-609-090-7	Sequence 7, Appl
34	55	100.0	39	2 US-08-682-245A-1	Sequence 1, Appl
35	55	100.0	39	2 US-08-682-245A-1	Sequence 1, Appl
36	55	100.0	40	1 US-07-744-767A-37	Sequence 2, Appl
37	55	100.0	40	1 US-08-235-400-2	Sequence 1, Appl
38	55	100.0	40	1 US-08-476-464A-2	Sequence 2, Appl
39	55	100.0	40	1 US-08-304-585-1	Sequence 1, Appl
40	55	100.0	40	1 US-08-302-808-3	Sequence 3, Appl
41	55	100.0	40	2 US-08-433-734-1	Sequence 1, Appl
42	55	100.0	40	2 US-08-609-090-8	Sequence 8, Appl
43	55	100.0	40	2 US-07-737-371E-69	Sequence 69, Appl
44	55	100.0	40	2 US-08-682-245A-2	Sequence 2, Appl
45	55	100.0	40	2 US-08-986-948-3	Sequence 3, Appl
46	55	100.0	40	2 US-08-461-216-1	Sequence 1, Appl
47	55	100.0	40	4 US-08-959-148-1	Sequence 1, Appl
48	55	100.0	40	4 US-09-242-724-22	Sequence 22, Appl
49	55	100.0	40	4 US-08-723-661B-1	Sequence 1, Appl
50	55	100.0	40	5 PCT-US92-06700-1	Sequence 1, Appl

RESULT 1

US-08-612-785B-37
Sequence 37, Application US/08612785B
Patent No. 5854204

GENERAL INFORMATION:

APPLICANT: Findexis, Mark A. et al.

TITLE OF INVENTION: Ab peptides that modulate b-Amyloid

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESS: LAHIVE & COCKFIELD

STREET: 28 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,785B

FILING DATE: Herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/404,831

FILING DATE: 14-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/475,579

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/548,998

FILING DATE: 27-OCT-1995

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A.

REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: PPI-002CP3

TELEPHONE: (617)1227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-7858-37

Query Match 100.0%; Score 55; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
Db 3 HHOKLVFFAE 12

RESULT 2
US-09-264-709A-2
Sequence 2, Application US/09264709A
Patent No. 6320024
GENERAL INFORMATION:
APPLICANT: Roberts, Eugene
TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
FILE REFERENCE: 2124-310
CURRENT APPLICATION NUMBER: US/09/264,709A
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: 08/797,782
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-264-709A-2

Query Match 100.0%; Score 55; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
Db 2 HHOKLVFFAE 11

RESULT 3
US-08-304-585-7
Sequence 7, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Maggio, John E.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muehling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muehling, Ann M.
REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 110.00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-7

Query Match 100.0%; Score 55; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
Db 4 HHOKLVFFAE 13

RESULT 4
US-08-346-849-4
Sequence 4, Application US/08346849
Patent No. 5670483
GENERAL INFORMATION:
APPLICANT: Zhang, Shuangang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-346-849-4

Query Match 100.0%; Score 55; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
13 HHOKLVFFAE 22

RESULT 5

US-08-302-808-7
; Sequence 7, Application US/08302808
; Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhltro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-7

Query Match 100.0%; Score 55; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHOKLVFFAE 10
13 HHOKLVFFAE 22

RESULT 6

US-08-609-090-2
; Sequence 2, Application US/08609090
; Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-2

Query Match 100.0%; Score 55; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
13 HHOKLVFFAE 22

RESULT 7

US-08-986-948-7
; Sequence 7, Application US/08986948
; Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uhltro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-7

Query Match      100.0%; Score 55; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

RESULT 8
US-08-293-284A-4
Sequence 4, Application US/08293284A
Patent No. 5955343
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shungang
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: TWO MILLITIA DRIVE
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-284A-4

Query Match      100.0%; Score 55; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

RESULT 9
US-08-461-216-2
Sequence 2, Application US/08461216
Patent No. 5958883
GENERAL INFORMATION:
APPLICANT: Snow, A.D.
TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,216
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,734
FILING DATE: October 23, 1992
APPLICATION NUMBER: 07/950,417
FILING DATE: September 23, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: UOFW-1-6707
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
TELEFAX: 1-206-224-0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: (SYMBOL 98 \f "Symbol")/AA(1-28);
DESCRIPTION: page 83, line 31
US-08-461-216-2

Query Match
Best Local Similarity 100.0%; Score 55; DB 2; Length 28;
Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
DB 13 HHOKLVFAE 22

RESULT 10
US-09-388-890-2

Sequence 2, Application US/09388890
Patent No. 6136548
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
CLASSIFICATION:
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/686,959
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
IMMEDIATE SOURCE:
CLONE: B(1-28) peptide of amyloid B protein
US-09-388-890-2

Query Match
Best Local Similarity 100.0%; Score 55; DB 4; Length 28;
Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
DB 13 HHOKLVFAE 22

RESULT 11
US-09-388-890-3

Sequence 3, Application US/09388890
Patent No. 6136548
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
CLASSIFICATION:
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/686,959
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
IMMEDIATE SOURCE:
CLONE: DIN B(1-28) peptide of amyloid B protein
US-09-388-890-3

Query Match
Best Local Similarity 100.0%; Score 55; DB 4; Length 28;
Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
DB 13 HHOKLVFAE 22

RESULT 12
US-09-388-890-4

Sequence 4, Application US/09388890
Patent No. 6136548
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
CLASSIFICATION:
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/686,959
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
IMMEDIATE SOURCE:
CLONE: DIN B(1-28) peptide of amyloid B protein
US-09-388-890-4

Query Match
Best Local Similarity 100.0%; Score 55; DB 4; Length 28;
Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
DB 13 HHOKLVFAE 22

COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,890
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/686,959
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
IMMEDIATE SOURCE:
CLONE: E3Q B(1-28) peptide of amyloid B protein
US-09-388-890-4

Query Match 100.0%; Score 55; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
|||
Db 13 HHOKLVFFAE 22

RESULT 13
US-09-388-890-5
Sequence 5, Application US/09388890
Patent No. 6136548
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
TITLE OF INVENTION: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,890
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/686,959
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.

REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
IMMEDIATE SOURCE:
CLONE: R5Q B(1-28) peptide of amyloid B protein
US-09-388-890-5

Query Match 100.0%; Score 55; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
|||
Db 13 HHOKLVFFAE 22

RESULT 14
US-09-388-890-6
Sequence 6, Application US/09388890
Patent No. 6136548
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
TITLE OF INVENTION: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,890
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/686,959
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
IMMEDIATE SOURCE:
CLONE: H6Q B(1-28) peptide of amyloid B protein

US-09-388-890-6

Query Match 100.0%; Score 55; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
|||||
DB 13 HHOKLVFAE 22

RESULT 15

US-09-388-890-7
; Sequence 7, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/388,890
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,959
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; IMMEDIATE SOURCE:
; CLONE: D7Q B(1-28) peptide of amyloid B protein
; US-09-388-890-7

Query Match 100.0%; Score 55; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
|||||
DB 13 HHOKLVFAE 22

RESULT 16
US-09-388-890-8
; Sequence 8, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:

APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/388,890
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,959
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; IMMEDIATE SOURCE:
; CLONE: E11Q B(1-28) peptide of amyloid B protein
; US-09-388-890-8

Query Match 100.0%; Score 55; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
|||||
DB 13 HHOKLVFAE 22

RESULT 17
US-09-388-890-13
; Sequence 13, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,890
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/686,959
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
IMMEDIATE SOURCE:
CLONE: D23Q B(1-28) peptide of amyloid B protein

Query Match 100.0%; Score 55; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHOKLVFFAE 10
Db 13 HHOKLVFFAE 22

RESULT 18
US-09-388-890-14
Sequence 14, Application US/09388890
Patent No. 6136548
GENERAL INFORMATION:
APPLICANT: ANDERSON, STEPHEN
TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
TITLE OF INVENTION: OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,890
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/686,959
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
IMMEDIATE SOURCE:
CLONE: K28Q B(1-28) peptide of amyloid B protein

Query Match 100.0%; Score 55; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHOKLVFFAE 10
Db 13 HHOKLVFFAE 22

RESULT 19
US-09-264-709A-1
Sequence 1, Application US/09264709A
Patent No. 6320024
GENERAL INFORMATION:
APPLICANT: Roberts, Eugene
TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
TITLE OF INVENTION: Improve the Quality of Life
FILE REFERENCE: 2124-310
CURRENT APPLICATION NUMBER: US/09/264,709A
CURRENT FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: 08/797,782
PRIOR FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
US-09-264-709A-1

Query Match 100.0%; Score 55; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHOKLVFFAE 10
Db 13 HHOKLVFFAE 22

RESULT 20
US-08-723-661B-2
Sequence 2, Application US/08723661B
Patent No. 6340783
GENERAL INFORMATION:
APPLICANT: Alan D Snow
TITLE OF INVENTION: Animal Models of Human Amyloidosis
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrick M. Dwyer
STREET: 1818 Westlake Avenue N, Suite 114
CITY: Seattle
STATE: WA (Washington)
COUNTRY: United States of America
ZIP: 98109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS (Windows 98)
SOFTWARE: WordPerfect 5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,661B
FILING DATE: 31-Oct-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,216
FILING DATE: 05-Jun-1995
APPLICATION NUMBER: 07/969,734
FILING DATE: 23-Oct-1992
APPLICATION NUMBER: 07/950,417
FILING DATE: 23-Sep-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dwyer, Patrick M.
REGISTRATION NUMBER: 32,411
REFERENCE/DOCKET NUMBER: PROTEO.P00C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 343-7074
TELEFAX: (206) 343-7085
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
DESCRIPTION: /A4 (1-28); page 83, line 31
US-08-723-661B-2
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match
Best Local Similarity 100.0%; Score 55; DB 4; Length 28;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
|||||
Db 13 HHOKLVFFAE 22

RESULT 21
US-08-609-090-3
Sequence 3, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1124
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-3

Query Match
Best Local Similarity 100.0%; Score 55; DB 2; Length 30;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
|||||
Db 13 HHOKLVFFAE 22

RESULT 22
US-08-609-090-4
Sequence 4, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1124
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-4

Query Match
Best Local Similarity 100.0%; Score 55; DB 2; Length 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
|||||
Db 13 HHOKLVFFAE 22

RESULT 23
US-08-304-585-6
Sequence 6, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Maggio, John E.

APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muelting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 561415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muelting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-6

Query Match 100.0%; Score 55; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
DB 13 HHOKLVFAE 22

RESULT 24
US-08-612-7858-36
Sequence 36, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPT-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-7858-36

Query Match 100.0%; Score 55; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
DB 8 HHOKLVFAE 17

RESULT 25
US-08-612-7858-38
Sequence 38, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPT-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-38

Query Match 100.0%; Score 55; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

RESULT 26
US-08-612-785B-40
Sequence 40, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:

APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESSES:
ADDRESS: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConli, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PRI-0020C3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-40

Query Match 100.0%; Score 55; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

DB 8 HHOKLVFFAE 17

RESULT 27
US-08-609-090-6
Sequence 6, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:

APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESS: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-6

Query Match 100.0%; Score 55; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

RESULT 28
US-08-302-808-1
Sequence 1, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:

APPLICANT: SUZUKI, No. 5750349uhlro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESS: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA

Query Match 100.0%; Score 55; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-1

Query Match 100.0%; Score 55; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
Db 13 HHOKLVFFAE 22

RESULT 29
US-07-737-371E-68
Sequence 68, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-68

Query Match 100.0%; Score 55; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
Db 13 HHOKLVFFAE 22

RESULT 30
US-08-986-948-1
Sequence 1, Application US/08986948
Patent No. 595317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uh1ro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S

REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-1

Query Match 100.0%; Score 55; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
|||||
Db 13 HHOKLVFFAE 22

RESULT 31
US-08-304-585-5
Sequence 5, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Magglio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muetling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muetling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00010120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-5

Query Match 100.0%; Score 55; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
|||||
Db 12 HHOKLVFFAE 21

RESULT 32
US-08-302-808-2
Sequence 2, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uh1to
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-2

Query Match 100.0%; Score 55; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
|||||
Db 13 HHOKLVFFAE 22

RESULT 33
US-08-609-090-7
Sequence 7, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: KRAUS, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-7
Query Match 100.0%; Score 55; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHOKLVFFAE 10
Db 13 HHOKLVFFAE 22
RESULT 34
US-08-682-245A-1
Sequence 1, Application US/08682245A
Patent No. 5919631
GENERAL INFORMATION:
APPLICANT: GOYAL, SHEPALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHARABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE BAA PEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A.
ZIP: 45215-6300

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L.
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-1
Query Match 100.0%; Score 55; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHOKLVFFAE 10
Db 13 HHOKLVFFAE 22
RESULT 35
US-08-986-948-2
Sequence 2, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317unlro
APPLICANT: KITADA, Chioko
APPLICANT: ODAKA, Asano
TITLE OF INVENTION: ANTIBODIES TO B-AMYLIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993

FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-2

Query Match 100.0%; Score 55; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
|||||
Db 13 HHOKLVFFAE 22

RESULT 36
US-07-744-767A-1
Sequence 1, Application US/07744767A
Patent No. 5434050
GENERAL INFORMATION:
APPLICANT: Maglio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: Labelled
TITLE OF INVENTION: for use in Detecting Alzheimer's Disease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner, P.A.
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/744,767A
FILING DATE: 13-AUG-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueeling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 600,226-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-07-744-767A-1
Query Match 100.0%; Score 55; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
|||||
Db 13 HHOKLVFFAE 22

RESULT 37
US-08-235-400-2
Sequence 2, Application US/08235400
Patent No. 5552426
GENERAL INFORMATION:
APPLICANT: Lunn, William H.
APPLICANT: Monn, James A.
APPLICANT: Zimmerman, Dennis M.
TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL
TITLE OF INVENTION: DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/1104
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,400
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9507
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-235-400-2

Query Match 100.0%; Score 55; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
|||||
Db 13 HHOKLVFFAE 22

RESULT 38
US-08-476-464A-2
Sequence 2, Application US/08476464A
Patent No. 5707821
GENERAL INFORMATION:
APPLICANT: Rydel, Russell E.
APPLICANT: Dappen, Michael S.
TITLE OF INVENTION: THERAPEUTIC INHIBITION OF PHOSPHOLIPASE
TITLE OF INVENTION: A2 IN A-BETA PEPTIDE-MEDIATED NEURODEGENERATIVE DISEASE

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREY LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,464A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA, JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15270-002300
TELEPHONE: (415)326-2400
TELEFAX: (415)326-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-464A-2

Query Match 100.0%; Score 55; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
Db 13 HHOKLVFFAE 22

RESULT 39
US-08-304-585-1
Sequence 1, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Magglio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/304,585
FILING DATE: 12-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110,00010120
TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-304-585-1

Query Match 100.0%; Score 55; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
Db 13 HHOKLVFFAE 22

RESULT 40
US-08-302-808-3
Sequence 3, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349unh1ro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-3

Query Match 100.0%; Score 55; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

RESULT 41
US-08-433-734-1
Sequence 1, Application US/08433734
Patent No. 5837473
GENERAL INFORMATION:
APPLICANT: Maglio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: Labelled - Amyloid Peptide and Methods
TITLE OF INVENTION: for Use in Detecting Alzheimer's Disease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muehling, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 584415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,734
FILING DATE: 03-May-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muehling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00010102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1220
TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-433-734-1

Query Match 100.0%; Score 55; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

RESULT 42
US-08-609-090-8
Sequence 8, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: Hensley, Kenneth
APPLICANT: Butterfield, D. A.
APPLICANT: Carney, John M.

APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-8

Query Match 100.0%; Score 55; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

RESULT 43
US-07-737-371E-69
Sequence 69, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990

ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-69

Query Match 100.0%; Score 55; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

RESULT 44
US-08-682-245A-2
Sequence 2, Application US/08682245A
Patent No. 5919631
GENERAL INFORMATION:
APPLICANT: GOYAL, SHEFALI
APPLICANT: PAUL, JOSEPH W
APPLICANT: RIEDEL, NORBERT G
APPLICANT: SAHASRABUDHE, SUDHIR
TITLE OF INVENTION: A METHOD OF DETERMINING THE DEGREE OF
TITLE OF INVENTION: AGGREGATION OF THE B44 PEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOECHST MARION ROUSSEL, INC.
STREET: 2110 E. GALBRAITH RD., P.O. BOX 156300
CITY: CINCINNATI
STATE: OHIO
COUNTRY: U.S.A.
ZIP: 45215-6300
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,245A
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,414
FILING DATE: 16-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: LENTZ, NELSEN L
REGISTRATION NUMBER: 38,537
REFERENCE/DOCKET NUMBER: HR-1257A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 513-948-7369
TELEFAX: 513-948-7961 OR 4681
TELEX: 214320
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-682-245A-2

Query Match 100.0%; Score 55; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

RESULT 45
US-08-986-948-3
Sequence 3, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-3

Query Match 100.0%; Score 55; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFAE 10
13 HHOKLVFAE 22

RESULT 46

US-08-461-216-1
Sequence 1, Application US/08461216
Patent No. 595883
GENERAL INFORMATION:
APPLICANT: Snow, A.D.
TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSIS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,216
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,734
FILING DATE: October 23, 1992
APPLICATION NUMBER: 07/950,417
FILING DATE: September 23, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: UOFW-1-6707
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
TELEFAX: 1-206-224-0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: [SYMBOL 98 \f "Symbol"/A4(1-40);
US-08-461-216-1

Query Match 100.0%; Score 55; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFAE 10
13 HHOKLVFAE 22

RESULT 47
US-08-959-148-1
Sequence 1, Application US/08959148
Patent No. 6172277
GENERAL INFORMATION:
APPLICANT: Tate, Barbara A.
APPLICANT: Majocha, Ronald
APPLICANT: Newton, Julie L.
TITLE OF INVENTION: NON-TRANSGENIC ANIMAL MODEL OF ALZHEIMER'S DISEASE
FILE REFERENCE: 04930/022001

CURRENT APPLICATION NUMBER: US/08/959,148
CURRENT FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 40
TYPE: PPT
ORGANISM: Homo sapiens
US-08-959-148-1

Query Match 100.0%; Score 55; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFAE 10
13 HHOKLVFAE 22

RESULT 48
US-09-242-724-22
Sequence 22, Application US/09242724
Patent No. 6316405
GENERAL INFORMATION:
APPLICANT: Solomon, Michael E.
APPLICANT: Rich, Daniel H.

TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
FILE REFERENCE: Cyclosporin Analogs
CURRENT APPLICATION NUMBER: US/09/242,724
CURRENT FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 40
TYPE: PPT
ORGANISM: Homo sapiens
US-09-242-724-22

Query Match 100.0%; Score 55; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFAE 10
13 HHOKLVFAE 22

RESULT 49
US-08-723-661B-1
Sequence 1, Application US/08723661B
Patent No. 6340783
GENERAL INFORMATION:
APPLICANT: Alan D. Snow

TITLE OF INVENTION: Animal Models of Human Amyloidosis
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrick M. Dwyer
STREET: 1818 Westlake Avenue N, Suite 114
CITY: Seattle
STATE: WA (Washington)
COUNTRY: United States of America
ZIP: 98109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS (Windows 98)
SOFTWARE: WordPerfect 5.2

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,661B
FILING DATE: 31-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,216
FILING DATE: 05-Jun-1995

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; APPLICATION NUMBER: 07/969,734
; FILING DATE: 23-Oct-1992
; APPLICATION NUMBER: 07/950,417
; FILING DATE: 23-Sep-1992
; ATTORNEY/AGENT INFORMATION:
;   NAME: Dwyer, Patrick M.
;   REGISTRATION NUMBER: 32,411
;   REFERENCE/DOCKET NUMBER: PROTO.P00C1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 343-7074
;   TELEFAX: (206) 343-7085
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 40 AMINO ACIDS
;     TYPE: AMINO ACID
;     STRANDEDNESS: SINGLE
;     TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION: /A4 (1-40); FIGURES 23-29
; US-08-723-661B-1

```

```

Query Match      100.0%; Score 55; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 HHOKLVFFAE 10
    |||||||
Db 13 HHOKLVFFAE 22

```

RESULT 50

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PCT-US92-06700-1
; Sequence 1, Application PC/TUS9206700
; GENERAL INFORMATION:
;   APPLICANT: Mantyh, Patrick W.
;   APPLICANT: Magglio, John E.
;   TITLE OF INVENTION: Labelled -Amyloid Peptide
;   TITLE OF INVENTION: and Alzheimer's Disease Detection
;   NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Merchant & Gould
;   STREET: 3100 Northwest Center
;   CITY: Minneapolis
;   STATE: Minnesota
;   COUNTRY: USA
;   ZIP: 55402
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.5 inch, 720 KB
;   COMPUTER: Northgate 386
;   OPERATING SYSTEM: DOS 4.0
;   SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US92/06700
;   FILING DATE: 19920810
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kowalchuk, Alan W.
;   REGISTRATION NUMBER: 31,535
;   REFERENCE/DOCKET NUMBER: 600.226-WO-01
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (612) 332-5300
;   TELEFAX: (612) 332-9081
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 40 amino acid residues
;     TYPE: AMINO ACID
;     TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal Fragment
; ORIGINAL SOURCE: Synthetically Derived
; FEATURE:
;   NAME/KEY: Internal fragment of the

```

```

; NAME/KEY: amyloid peptide precursor
; LOCATION: Represents isolated internal
; LOCATION: sequence of 40 amino acid residues from
; LOCATION: the -amyloid peptide precursor
PCT-US92-06700-1
Query Match      100.0%; Score 55; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 HHOKLVFFAE 10
    |||||||
Db 13 HHOKLVFFAE 22

```

```

Search completed: October 29, 2002, 09:25:38
Job time : 14 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 09:23:27 ; Search time 16 Seconds
(without alignments)
60.056 Million cell updates/sec

Title: US-09-724-842a-27
Sequence: 1 HHOKLVFFAE 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: PIR_71:*

1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	42	2	PN0512
2	55	100.0	57	2	E60045
3	55	100.0	57	2	E60045
4	55	100.0	57	2	E60045
5	55	100.0	57	2	E60045
6	55	100.0	57	2	E60045
7	55	100.0	57	2	E60045
8	55	100.0	57	2	E60045
9	55	100.0	57	2	E60045
10	55	100.0	57	2	E60045
11	55	100.0	57	2	E60045
12	55	100.0	57	2	E60045
13	55	100.0	57	2	E60045
14	55	100.0	57	2	E60045
15	55	100.0	57	2	E60045
16	55	100.0	57	2	E60045
17	55	100.0	57	2	E60045
18	55	100.0	57	2	E60045
19	55	100.0	57	2	E60045
20	55	100.0	57	2	E60045
21	55	100.0	57	2	E60045
22	55	100.0	57	2	E60045
23	55	100.0	57	2	E60045
24	55	100.0	57	2	E60045
25	55	100.0	57	2	E60045
26	55	100.0	57	2	E60045
27	55	100.0	57	2	E60045
28	55	100.0	57	2	E60045
29	55	100.0	57	2	E60045

30	35	63.6	552	2	T25496	hypothetical prote
31	35	63.6	751	2	D71860	probable outer mem
32	35	63.6	850	2	JC5047	ras GTPase-activat
33	35	63.6	2347	1	TVHURS	kinase-related pro
34	34	61.8	124	1	B54546	small peptidoglyca
35	34	61.8	140	2	C81176	hypothetical prote
36	34	61.8	270	2	AG1727	hypothetical prote
37	34	61.8	281	2	AG1357	unknown protein hom
38	34	61.8	590	2	F95853	unknown proteins ho
39	34	61.8	635	2	H81793	probable phospholip
40	34	61.8	763	2	S51300	hypothetical prote
41	34	61.8	1163	2	S07137	probable membrane
42	34	61.8	1356	2	S51389	DNA-directed RNA p
43	34	61.8	1375	2	T18961	ROM2 protein - yea
44	34	61.8	4427	2	PN0637	polyketide synthas
45	33	60.0	214	2	S39644	acetone utilizatio
46	33	60.0	255	2	S41511	Brn-3a protein - m
47	33	60.0	258	2	D72217	conserved hypothet
48	33	60.0	325	2	A47003	cytokine receptor
49	33	60.0	334	2	T20562	hypothetical prote
50	33	60.0	336	2	S32170	phytoene synthetas

ALIGNMENTS

RESULT 1
PN0512
beta-amyloid protein - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PN0512
R:Shimohiyashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamlya, H.; Ohno
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra
A:Reference number: PN0512; MUID:93290653
A:Accession: PN0512
A:Molecule type: protein
A:Residues: 1-42 <SHI>
A:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinas
C:Keywords: alternative splicing; amyloid

Query Match 100.0%; Score 55; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

RESULT 2
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <IOH>
A:Cross-references: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinas
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 55; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10

Db 18 HHOKLVFFAE 27

RESULT 3

Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C:Accession: F60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079
 C:Accession: F60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56127; NID:91895; PIDN:CAI39592.1; PID:91896
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 55; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
 Db 18 HHOKLVFFAE 27

RESULT 4

Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: G60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079
 C:Accession: G60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56126
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 55; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
 Db 18 HHOKLVFFAE 27

RESULT 5

Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: D60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079
 C:Accession: D60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56124
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 55; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
 Db 18 HHOKLVFFAE 27

RESULT 6

Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: A60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A:Reference number: A60045; MUID:92017079
 C:Accession: A60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56125
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 55; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
 Db 18 HHOKLVFFAE 27

RESULT 7

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
 C:Species: Ursus maritimus (polar bear)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C:Accession: B60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A>Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A:Reference number: A60045; MUID:92017079
 C:Accession: B60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAI39593.1; PID:92166
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 55; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
 Db 18 HHOKLVFFAE 27

RESULT 8

Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
 C:Accession: P00438; C60045
 R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Marcoun, L.E.
 Biochem. Biophys. Res. Commun. 188, 905-911, 1992
 A>Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
 A:Reference number: P00438; MUID:93075180
 C:Accession: P00438
 A:Molecule type: DNA

A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 55; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFEAE 10
|||||
Db 29 HHOKLVFEAE 38

RESULT 9
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A:Accession: A49795
R:Podlasky, M.B.; Tolian, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a F
A:Reference number: A49795; MUID:91273117
A:Accession: A49795
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing

Query Match 100.0%; Score 55; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFEAE 10
|||||
Db 609 HHOKLVFEAE 618

RESULT 10
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
A:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 100.0%; Score 55; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFEAE 10

Db 661 HHOKLVFEAE 670
|||||
RESULT 11
OR004
Alzheimer's disease amyloid beta protein precursor (validated) - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inh
N:Contents: Amyloid beta protein long, plaque form; amyloid beta protein short, vascu
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
A:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562;
4668; A28583; A29302; A60805; J10038; S06121; A60355; A59011; A38384; S29076; S38252;
R:Lemaire, H.G.; Salbaum, J.M.; Multhaupt, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encode
A:Reference number: S02260; MUID:89128427
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: EMBL:X13466
A>Note: alternative splice form APP(695)
R:Lemaire, H.G.
Submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CAA13830.1; PID:g871360
A>Note: alternative splice form APP(695)
R:La Fauti, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-pr
A:Reference number: A32277; MUID:89165870
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAIC13654.1; PID:g516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simila
A:Reference number: A33260; MUID:89392030
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R:Prelli, F.; Levy, E.; Van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
A:Reference number: A35486; MUID:90321244
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A>Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318
A:Accession: I39452
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:g178613; PIDN:AAB55502.1; PID:g178616
A:Accession: I39451
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB/
A:Molecule type: DNA
A:Residues: 1-530, 'OWIMPIVPAFWKAVGR' <YOS2>
A:Cross-references: GB:M34875; NID:g178608; PIDN:AAB59501.1; PID:g178615
R:Yoshikaki, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168
A:Contents: annotation; erratum

A:Note: revised physical map for reference 139451
Riley, E.; Caman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen
Science 248, 1124-1126, 1990
A>Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrhage
A:Reference number: 139453; MUID:90260663
A:Accession: 139453
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A:Note: a mutation with 693-Gln is presented
Science 254, 97-99, 1991
A>Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A:Reference number: 159562; MUID:92022553
A:Accession: 159562
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:g236720; PIDN:ABD19991.1; PID:g236721
A:Note: K.; Orr, H.T.; Payami, H.; Wiseman, E.M.; Alonso, M.E.; Pullst, S.M.; Anderson,
Arakts, S.E.; Kornberg, J.R.; Sharma, V.; Kukull, W.; Larson, M.E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A>Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <RAM>
A:Cross-references: GB:S45135; NID:g257377; PIDN:AA23645.1; PID:g257378
A:Experimental source: familial Alzheimer disease family SB
A:Note: sequence extracted from NCBI backbone (NCBIP:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAN2>
A:Cross-references: GB:S45136; NID:g257379; PIDN:AA23646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family LIT
A:Note: this sequence has a silent mutation
R.Kang, J.; Lemaire, H.G.; Untebeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A>Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A:Reference number: A03134; MUID:87144572
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:U00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A:Note: alternative splice form APP(695)
R.Robakts, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A>Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A
A:Reference number: A29030; MUID:87231971
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R.Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Safiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A>Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M5533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A:Experimental source: brain
R.Tanzl, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A>Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TAN1>
A:Cross-references: GB:M5532; NID:g177957; PIDN:AAA51564.1; PID:g177958

R.D.Vyks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue
EMBO J. 7, 949-957, 1988
A>Title: Identification of transmembrane orientation and biogenesis of the amyloid A4 p
A:Reference number: S02638; MUID:86296437
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
Nature 331, 528-530, 1988
A>Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
A:Reference number: S00707; MUID:86122640
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'T', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:G28817; PIDN:CA030042.1; PID:G929612
A:Experimental source: promyelocytic leukemia cell line HL60
A>Note: alternative splice form AP(751)
R.Ponte, P.; Gonzalez-Demhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;
Nature 331, 525-527, 1988
A>Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh
A:Reference number: S00925; MUID:86122639
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-34, 'T', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:Y00297; NID:G28720; PIDN:CA030050.1; PID:G28721
A>Note: alternative splice form AP(751)
R.Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A>Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inh
A:Reference number: A38949; MUID:86122641
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:G28816; PIDN:CA030041.1; PID:G929611
A:Experimental source: glioblastoma cell line
A>Note: alternative splice form AP(770)
R.Vitek, M.P.; Rasooli, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashl
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A>Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 506-770 <VIT3>
R.Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A>Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
A:Reference number: A31087; MUID:86124954
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAT>
A:Cross-references: GB:M18734; NID:G178572; PIDN:AAA51726.1; PID:G178573
A>Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
A>Note: the cited Genbank accession number, J03594, is not in release 101.0
R.Masters, C.L.; Multhaup, G.; Simms, G.; Pottinger, J.; Martins, R.N.; Beyreuther,

RESULT 12

S23094
beta-amyloid protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S23094
R:Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A:Reference number: S23094; MUID:92316198
A:Accession: S23094
A:Molecule type: protein
A:Residues: 1-33 <KOJ>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

Query Match 85.5%; Score 47; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0099;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVEFAE 10
DB 19 HOKLVEFAE 27

RESULT 13

A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
M:Alternate names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sasaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor
A:Reference number: A27485; MUID:88106489
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M18373; NID:9191568; PIDN:AAA37139.1; PID:9309085
A:Experimental source: brain
R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochem. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A:Reference number: S19727; MUID:92096458
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: EMBL:X59379
R:Izumii, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sasaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A:Reference number: I49485; MUID:92209998
A:Accession: I49485
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D10603; NID:9220328; PIDN:BA01456.1; PID:9220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 85.5%; Score 47; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVEFAE 10
DB 610 HOKLVEFAE 618

RESULT 14

S00550

Alzheimer's disease amyloid beta protein precursor - rat
M:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hildlich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat br
A:Reference number: S00550; MUID:88312583
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:955616; PIDN:CAA30488.1; PID:955617
R:Schubert, D.; Schroeder, R.; Lacobiere, M.; Satch, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan co
A:Reference number: A41245; MUID:88264430
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A>Note: evidence for heparan sulfate attachment
R:Heese, L.; Behr, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627
A:Contents: annotation; copper binding sites
A>Note: rat peptides were isolated but not sequenced
R:Potemski, A.; Styles, J.; Menta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat b
A:Reference number: A39820; MUID:91217087
A:Accession: A39820
A>Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:65-648/Domain: transmembrane #status predicted <TM>

Query Match 85.5%; Score 47; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVEFAE 10
DB 610 HOKLVEFAE 618

RESULT 15

H64118
4-alpha-glucanotransferase homolog - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: H64118
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kinkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95550650
A:Accession: H64118
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-699 <TIGR>
A:Cross-references: GB:U32815; GB:I42023; NID:91574818; PIDN:AAC23003.1; PID:91574819
C:Genetics:
A:Start codon: GTG
C:Superfamily: 4-alpha-glucanotransferase

Query Match 70.9%; Score 39; DB 2; Length 699;
Best Local Similarity 66.7%; Pred. No. 9.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVEFA 9
|||||: |||
DB 349 HHOKLVEFA 357

RESULT 16

F70979

hypothetical protein RV3277 - Mycobacterium tuberculosis (strain H37RV)

C/Species: Mycobacterium tuberculosis

C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C/Accession: F70979

R/Colo: S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A/Reference number: A70500; MIMD:98295987

A/Accession: F70979

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-272 <COL>

A/Cross-references: GB:AE00476; GB:AL123456; NID:g3242259; PIDN:CAB07080.1; PID:e306544;

A/Experimental source: strain H37RV

C/Genetics: RV3277

A/Gene: RV3277

Query Match 69.1%; Score 38; DB 2; Length 272;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVEFA 9
|||||: |||
DB 137 HHOKLVEFA 145

RESULT 17

NUDC

glucose-6-phosphate isomerase (EC 5.3.1.9) - Escherichia coli

N/Alternate names: phosphoglucose isomerase; phosphohexose isomerase

C/Species: Escherichia coli

C/Date: 31-Mar-1990 #sequence_revision 17-Oct-1997 #text_change 08-Sep-2000

C/Accession: H6509; JS0142; S04396

R/Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MIMD:97426617

A/Accession: H6509

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-549 <BLAT>

A/Cross-references: GB:AE000476; GB:U00096; NID:g1790456; PIDN:AAC76995.1; PID:g1790457;

R/Froman, B.E.; Taft, R.C.; Gottlieb, L.D.

Mol. Gen. Genet. 217, 126-131, 1999

A/Title: Isolation and characterization of the phosphoglucose isomerase gene from Escher

A/Reference number: JS0142; MIMD:89364675

A/Accession: JS0142

A/Molecule type: DNA

A/Residues: 1-316, 'V', 318-549 <FRO>

A/Cross-references: GB:X15196; NID:g42376; PIDN:CAA33368.1; PID:g42377

A/Experimental source: strain JM101

A/Note: the authors translated the codon CAG for residue 8 as Trp

C/Comment: This enzyme catalyzes the reversible isomerization of glucose-6-phosphate and

C/Genetics: pgl

A/Map position: 91 min

C/Superfamily: glucose-6-phosphate isomerase

C/Keywords: glycolysis; homodimer; intramolecular oxidoreductase; isomerase
F/514/Active site: Lys #status predicted

Query Match 69.1%; Score 38; DB 1; Length 549;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
|||||: |||
DB 416 HHOKLV--FFAE 427

RESULT 18

H91254

glucosphosphate isomerase [imported] - Escherichia coli (strain O157:H7, substrain R

C/Species: Escherichia coli

C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C/Accession: H91254

R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C

gasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and 9

A/Reference number: A99629; MIMD:21156231; PMID:11258796

A/Accession: H91254

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-549 <NAV>

A/Cross-references: GB:BA000007; PIDN:BA38431.1; PID:g13364485; GSPDB:GN00154

A/Experimental source: strain O157:H7, substrain RIMD 0509952

C/Genetics:

A/Gene: ECS5008

C/Superfamily: glucose-6-phosphate isomerase

Query Match 69.1%; Score 38; DB 2; Length 549;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
|||||: |||
DB 416 HHOKLV--FFAE 427

RESULT 19

D86095

glucosphosphate isomerase [imported] - Escherichia coli (strain O157:H7, substrain E

C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C/Accession: D86095

R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

Miller, L.; Grobeck, E.J.; Davis, N.W.; Llm, A.; Dimalanta, E.; Potamousis, K.; Apoda

Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A83480; MIMD:21074935; PMID:11206551

A/Accession: D86095

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-549 <STO>

A/Cross-references: GB:AE005174; NID:g12518968; PIDN:AAG59224.1; GSPDB:GN00145; UMGF:

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A/Gene: pgl

C/Superfamily: glucose-6-phosphate isomerase

Query Match 69.1%; Score 38; DB 2; Length 549;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
|||||: |||
DB 416 HHOKLV--FFAE 427

RESULT 20

AD1013
 glucose-6-phosphate isomerase (EC 5.3.1.9) [imported] - *Salmonella enterica* subsp. enterica
 C:Species: *Salmonella enterica* subsp. *enterica* serovar *typhi*
 A:Note: this species has also been called *Salmonella typhi*
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AD1013
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Croft, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A:Authors: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Croft, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
 A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AD1013
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-549 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD09205.1; PID:gl6505209; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY4417
 C:Superfamily: glucose-6-phosphate isomerase
 C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 69.1%; Score 38; DB 2; Length 549;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
 ||||| |||
 DB 416 HHOKLSNFFAQ 427

RESULT 21
 B82330
 glucose-6-phosphate isomerase VC0374 [imported] - *Vibrio cholerae* (strain N16961 serogroup C)
 C:Species: *Vibrio cholerae*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: B82330
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Charidson, D.; Esmolaeva, M.D.; Vamathavan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.L.R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A:Reference number: AB2035; PMID:20406833
 A:Accession: B82330
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-550 <HEI>
 A:Cross-references: GB:AE004126; GB:AE003852; NID:g9654802; PIDN:AAF93547.1; GSPDB:GN001
 C:Genetics:
 A:Map position: 1
 C:Superfamily: glucose-6-phosphate isomerase

Query Match 69.1%; Score 38; DB 2; Length 550;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
 ||||| |||
 DB 417 HHOKLSNFFAQ 428

RESULT 22
 T04853
 hypothetical protein F28A21.20 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
 C:Accession: T04853
 R:Bevan, M.; Mueller, M.W.; Muendlein, A.; Feilber, R.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999
 A:Reference number: Z15387

A:Accession: T04853
 A:Molecule type: DNA
 A:Residues: 1-191 <BEV>
 A:Cross-references: EMBL:AL035526
 A:Experimental source: cultivar Columbia; BAC clone F28A21
 C:Genetics:
 A:Map position: 4
 A:Note: F28A21.20
 C:Superfamily: *Arabidopsis thaliana* hypothetical protein F28A21.20

Query Match 67.3%; Score 37; DB 2; Length 191;
 Best Local Similarity 60.0%; Pred. No. 6.1;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
 ||| |||
 DB 86 HHQACVFFCQ 95

RESULT 23
 I58391
 sarcoma amplified sequence SAS [imported] - human
 C:Species: *Homo sapiens* (man)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
 C:Accession: I58391
 R:Jankowski, S.A.; Mitchell, D.S.; Smith, S.H.; Trent, J.M.; Meltzer, P.S.
 Oncogene 9, 1205-1211, 1994
 A:Title: SAS, a gene amplified in human sarcomas, encodes a new member of the transmembrane
 A:Reference number: I58391; PMID:94181273
 A:Accession: I58391
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-210 <RES>
 A:Cross-references: EMBL:U01160; NID:g457936; PIDN:AA17782.1; PID:g457937
 C:Genetics:
 A:Gene: GDB:SAS
 A:Cross-references: GDB:128054; OMIM:181035
 A:Map position: 12q13-12q14

Query Match 65.5%; Score 36; DB 2; Length 210;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVFF 8
 ||| |||
 DB 70 HHQVLEFF 77

RESULT 24
 S51577
 transposase - rice blast fungus
 C:Species: *Magnaporthe grisea* (rice blast fungus)
 C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Sep-1997
 C:Accession: S51577
 R:Kachroo, P.; Leong, S.A.; Chattoo, B.B.
 Mol. Gen. Genet. 245, 339-348, 1994
 A:Title: Pot2, an inverted repeat transposon from the rice blast fungus *Magnaporthe grisea*
 A:Reference number: S51577; PMID:9511565
 A:Accession: S51577
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-535 <KAC>
 A:Cross-references: EMBL:Z33638; NID:g496853; PID:g496854

Query Match 65.5%; Score 36; DB 2; Length 535;
 Best Local Similarity 77.8%; Pred. No. 29;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 HOKLVFFAE 10
 ||| |||
 DB 80 HOKLVFFAE 88

RESULT 25
F69159
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: F69159
R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadefora, R.; Vialaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; M0ID:98037514
A:Accession: F69159
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-859 <MTH>
A:Cross-references: GB:AE000830; GB:AE000666; NID:g2621523; PIDN:AAB84962.1; PID:g262152
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH456
C:Keywords: lyase

Query Match 65.5%; Score 36; DB 2; Length 859;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HHOKLVEFA 9
||| |||
DB 210 HHQYLAIFYA 218

RESULT 26
C69224
C:Species: Methanobacterium thermoautotrophicum (strain Delta H)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: C69224
R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadefora, R.; Vialaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; M0ID:98037514
A:Accession: C69224
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1668 <MTH>
A:Cross-references: GB:AE000868; GB:AE000666; NID:g2622025; PIDN:AAB85426.1; PID:g262202
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH928
A:Start codon: GTG
C:Superfamily: Methanobacterium thermoautotrophicum cobalamn biosynthesis protein N

Query Match 65.5%; Score 36; DB 1; Length 1668;
Best Local Similarity 66.7%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HHOKLVEFA 9
||| |||
DB 792 HHQYLAIFYA 800

RESULT 27
T23909
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23909
R:Harris, B.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19816
A:Accession: T23909

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-297 <NLT>
A:Cross-references: EMBL:Z74475; PIDN:CAA98959.1; GSPDB:GN00023; CESP:R04F11.1
A:Experimental source: clone R04F11
C:Genetics:
A:Gene: CESP:R04F11.1
A:Map position: 5
A:Introns: 44/3; 82/3; 120/1; 156/1; 244/3

Query Match 63.6%; Score 35; DB 2; Length 297;
Best Local Similarity 55.6%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVEFA 9
||| |||
DB 157 HHKGVIFFA 165

RESULT 28
T50786

nucleoid DNA-binding protein cnd41-like protein - Arabidopsis thaliana

N:Alternate names: protein T30N20_40

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000

C:Accession: T50786

R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.;
submitted to the Protein Sequence Database, July 2000

A:Reference number: Z25240

A:Accession: T50786

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-446 <BEV>

A:Cross-references: EMBL:AL365234

A:Experimental source: cultivar Columbia; BAC clone T30N20

C:Genetics:

A:Map position: 5

A:Introns: 31/3; 173/1

A:Note: T30N20_40

Query Match 63.6%; Score 35; DB 2; Length 446;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HHOKLVEF 8
||| |||
DB 21 HHKHLVEF 28

RESULT 29
G84996

glucose-6-phosphate isomerase (EC 5.3.1.9) [Imported] - Buchnera sp. (strain APS)

C:Species: Buchnera sp.

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: G84996

R:Shenbrot, S.; Matanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp

A:Reference number: AB4930; M0ID:20445173

A:Accession: G84996

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-549 <STO>

A:Cross-references: GB:AP000398; GSPDB:GN00144

A:Experimental source: strain APS

C:Genetics:

A:Gene: pgi; B0573

C:Superfamily: glucose-6-phosphate isomerase

C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 63.6%; Score 35; DB 2; Length 549;
Best Local Similarity 58.3%; Pred. No. 47;
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

```

OY      1 HHQKLV--FEAE 10
          |||:..|||:
Db      416 HHMKLISNFFAQ 427

```

RESULT 30
T25496
hypothetical protein C03G6.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_reviation 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T25496
R:Murray, J.; Muhlmann, P.
submitted to the EMBL Data Library, April 1997
A:Description: The sequence of C. elegans cosmid C03G6.
A:Reference number: Z20042
A:Accession: T25496
A>Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: DNA
A:Residues: 1-552 <MOR>
A:Cross-references: EMBL:U97008; PIDN:AAH52105.1; GSPDB:GN00023; CESP:C03G6.5
A:Experimental source: strain Bristol N2; clone C03G6
C:Genetics:
A:Gene: CESP:C03G6.5
A:Map position: 5
A:Introns: 28/3; 75/3; 213/3; 330/1; 393/3

RESULT 31
D71860
Probable outer membrane protein - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C:Accession: D71860
R:Aln, R.A.; Ling, L.S.L.; Molr, D.T.; King, B.L.; Brown, E.D.; Doty, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Meberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; M0ID:59120557
A:Accession: D71860
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-751 <ARN>
A:Cross-references: GB:AE001529; GB:AE001439; NID:g4155590; PIDN:AAD06586.1; PID:g4155555
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp1008

```

RESULT 32
JC5047
ras GTPase-activating protein - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Nov-1999
C:Accession: JC5047
R: Kobayashi, M.; Masui, T.; Kusuda, J.; Kameoka, Y.; Hashimoto, K.; Iwashita, S.

```

Gene 175, 173-177, 1996
 A:Title: Human RasGTPase-activating protein (human counterpart of GAP1m): Sequence of
 A:Reference number: J05047; MUID:97074668
 A:Accession: J05047
 A:Molecule type: mRNA
 A:Residues: 1-850 <KOB>
 A:Cross-references: DDBJ:ID78155; NID:q1060908; PIDN:BA11230.1; PID:d1011892; PID:q10
 A:Comment: This protein plays a role in the regulation of cell growth and differentiat
 C:Genetics:
 A:Gene: GAP1m
 A:Map position: 3q24-26
 C:Superfamily: plectstrin repeat homology; ras-specific GAP catalytic domain homology
 F:355-568/Domain: ras-specific GAP catalytic domain homology <GAP>
 F:603-704/Domain: plectstrin repeat homology <PIK>

RESULT 33
TYROS
kinase-related protein *ros-1* precursor - human
MAlternate names: protein-tyrosine kinase *src* (activated *ros-1*)
MContains: protein-tyrosine kinase (EC 2.7.1.112) *ros-1*
CSpecies: Homo sapiens (man)
CDate: 31-Dec-1988 #sequence_revision 07-Oct-1994 #text_change 11-Jun-1999
CAccession: A35512; A25223; A24421; A33081
R.Birchmeier, C.; O'Neill, K.; Riggs, M.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 4799-4803, 1990
A>Title: Characterization of *ROS1* cDNA from a human glioblastoma cell line.
A.Reference number: A35512; MUID:90280463
A.Accession: A35512
A.Molecule type: mRNA
A.Residues: 1-2212, 'N', 2214-2227, 'QC', 2229-2347 <BIR>
A.Cross-references: GB:M34353
A.Experimental source: glioblastoma cell line SW-1088
R.Matsushime, H.; Wang, L.H.; Shibuya, M.
Mol. Cell. Biol. 6, 3000-3004, 1986
A>Title: Human *C-ros-1* gene homologous to the *v-ros* sequence of UR2 sarcoma virus enc
A.Reference number: A25223; MUID:87064611
A.Accession: A25223
A.Molecule type: DNA
A.Residues: 1790-2245, 'KEDSSSEFSFRCTVN' <MA2>
A.Cross-references: GB:M13368
A.Experimental source: placenta
A>Note: the differences after residue 2245 result from the authors' misinterpretation
R.Birchmeier, C.; Birnbaum, D.; Maitches, G.; Pasano, O.; Wigler, M.
Mol. Cell. Biol. 6, 3109-3116, 1986
A>Title: Characterization of an activated human *ros* gene.
A.Reference number: A24421; MUID:87064625
A.Accession: A24421
A.Molecule type: mRNA
A.Residues: 1854-2261, 'A', 2263-2347 <B12>
A.Cross-references: GB:M13880; NID:g337482; PION:AA35580.1; PID:g337483
A.Experimental source: tumor cells
A>Note: the *src* oncogene was formed by DNA rearrangement involving fusion of at leas
C.Genetics:
A.Gene: GDB:ROS1
A.Cross-references: GDB:120351; OMIM:165020
A.Map position: 6q22-6q22
C.Superfamily: C1881/L1: 1926/2; 1980/3; 2002/2; 2045/3; 2078/2; 2145/2; 2190/2
C.Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming prote
F/1-36/Domain: signal sequence #status predicted <SIG>
F/37-2347/Product: kinase-related protein *ROS1* #status predicted <MAT>
F/37-1859/Domain: extracellular #status predicted <EXT>
F/335-378/Domain: LDL receptor YWTD-containing repeat homology <YML>
F/466-503/Domain: LDL receptor YWTD-containing repeat homology <YMA>

F:715-757/Domain: LDL receptor YWTD-containing repeat homology <YW2>
 F:758-798/Domain: LDL receptor YWTD-containing repeat homology <YW3>
 F:799-838/Domain: LDL receptor YWTD-containing repeat homology <YW4>
 F:843-888/Domain: LDL receptor YWTD-containing repeat homology <YW5>
 F:893-933/Domain: LDL receptor YWTD-containing repeat homology <YW6>
 F:1532-1574/Domain: LDL receptor YWTD-containing repeat homology <YW7>
 F:1860-1883/Domain: Intramembrane #status predicted <TM>
 F:1884-2347/Domain: Intracellular #status predicted <INT>
 F:1943-2222/Domain: protein kinase homology <KIN>
 F:1951-1959/Region: protein kinase ATP-binding motif
 F:522-114,123,354,471,607,628,706,714,732,939,961,1015,1087,1090,1211,1272,1330,1458,
 F:1980/Active site: lys #status predicted
 F:2110,2114,2115/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #stat

Query Match 63.6%; Score 35; DB 1; Length 2347;
 Best Local Similarity 55.6%; Pred. NO. 2.1e+02;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHKLVFAE 10
 ||:|:|:|
 DB 333 HHQIVFSE 341

RESULT 34

Small peptidoglycan-associated lipoprotein sfp precursor - *Bacillus subtilis*
 N:Alternate names: PAL-related lipoprotein; peptidoglycan-associated lipoprotein homolog
 C:Species: *Bacillus subtilis*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Jun-2000
 C:Accession: B54546; D69708
 R:Hemlase, H.
 FEMS Microbiol. Lett. 66, 37-41, 1991

A:Title: Sequence of a PAL-related lipoprotein from *Bacillus subtilis*.
 A:Reference number: A54546; MUID:92038903
 A:Accession: B54546
 A:Molecule type: DNA

A:Residues: 1-124 <HEM>
 A:Experimental source: 168 strain BRB1

A:Note: sequence extracted from NCBI Backbone (NCBI:63826, NCBI:63828)
 R:Kunst, F.; Ogasawara, N.; Moser, A.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 A.; Bron, S.; Brouillette, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997

A:Authors: Foulger, D.R.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Gallizzi, A.; Gall
 Lech, J.; Hartwood, C.R.; Henuat, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinis,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y.M.; Ogawa, K.; Ogikawa, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadle, Y.; Sato, T.; Scanton,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
 A.; T. Miners, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Zanchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A65860; MUID:96044033

A:Accession: D69708
 A:Status: nucleic acid sequence not shown; translation not shown

A:Residues: 1-124 <KUN>
 A:Molecule type: DNA

A:Cross-references: GB:299111; GB:AL009126; NID:92633659; PIDN:CB1335.1; PID:92633633
 A:Experimental source: strain 168

C:Genetics:
 A:Gene: sfp

C:Superfamily: *Bacillus subtilis* small peptidoglycan-associated lipoprotein sfp
 C:Keywords: blocked amino end; lipoprotein

F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
 F:19/Modified site: fatty acylated amino end (Cys) (in mature form) #status predicted

Query Match 61.8%; Score 34; DB 1; Length 124;
 Best Local Similarity 40.0%; Pred. NO. 15;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 HHKLVFAE 10
 ||:|:|:|
 DB 36 HHQIVFSD 45

RESULT 35

hypothetical protein NMB0648 [imported] - *Neisseria meningitidis* (strain MC58 serogro
 C:Species: *Neisseria meningitidis*
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C:Accession: C61176
 R:Retzein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizza, M.
 Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunoli, R.;
 A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A:Reference number: A61000; MUID:2017575

A:Accession: C61176
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-140 <TEM>
 A:Cross-references: GB:AE002419; GB:AE002098; NID:97225863; PIDN:AAF1069.1; PID:9722

A:Experimental source: serogroup B, strain MC58
 C:Genetics:
 A:Gene: NMB0648

C:Superfamily: *Neisseria meningitidis* hypothetical protein NMB0648

Query Match 61.8%; Score 34; DB 2; Length 140;
 Best Local Similarity 50.0%; Pred. NO. 18;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HHKLVF 8
 ||:|:|:|
 DB 86 HHKLVF 93

RESULT 36

unknown protein homolog 1ln2364 [imported] - *Listeria innocua* (strain C11p1262)
 C:Species: *Listeria innocua*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C:Accession: AG1727
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsthl,
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kunz, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maltournam, A.;
 Ok, C.; Schueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A:Title: Comparative genomics of *Listeria species*.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AG1727
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-270 <GLN>
 A:Cross-references: GB:AL592022; PIDN:CA97591.1; PID:916414887; GSPDB:GN00178

A:Experimental source: strain C11p1262
 C:Genetics:

A:Gene: 1ln2364
 C:Superfamily: hypothetical protein ywpJ

Query Match 61.8%; Score 34; DB 2; Length 270;
 Best Local Similarity 60.0%; Pred. NO. 35;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HHKLVFAE 10
 ||:|:|:|
 DB 72 HHKLVFAE 81

RESULT 37

AG1357
 unknown proteins homolog 1mo2263 [imported] - *Listeria monocytogenes* (strain ESD-e)

C:Species: *Listeria monocytogenes*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AG1357
 R:Glaser, P.; Frangoul, L.; Buchliesser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fshl, H.; Jones, L.M.; Kerst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitouran, A.; Ma, O.K.; Schlueter, T.; Simoes, N.; Tlerraz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.; Title: Comparative genomics of *Listeria species*
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AG1357
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-281 <GLA>
 A:Cross-references: GB:NC_003210; PID:916411733; GSPDB:GN00177
 A:Experimental source: strain EGD-e
 C:Genetics:
 A:Gene: lmo2263

Query Match 61.8%; Score 34; DB 2; Length 281;
 Best Local Similarity 60.0%; Pred. No. 37;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 HHOKLVFAE 10
 ||:|:|:|
 Db 83 HHPRLTFAE 92

RESULT 38
 F95853
 Probable phospholipase protein [Imported] - *Sinorhizobium meliloti* (strain 1021) magapla
 C:Species: *Sinorhizobium meliloti*
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: F95853
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan, Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1,683-kb PSYMB megaplasmid from the N2-fixing endo
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: F95853
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-590 <KUN>
 A:Cross-references: GB:AL591985; PID:CA648494.1; PID:915139966; GSPDB:GN00167
 A:Experimental source: strain 1021, megaplasmid PSYMB
 R:Gallagher, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; LaLaurie, hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: SMD20094
 A:Genome: plasmid

Query Match 61.8%; Score 34; DB 2; Length 590;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLV 6
 |||||
 Db 208 HHOKLV 213

RESULT 39
 H81793
 Hypothetical protein NMA2205 [Imported] - *Neisseria meningitidis* (strain 22491 serogroup
 C:Species: *Neisseria meningitidis*
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: H81793

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
 ; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Kungall, K.; Quail, M.A.; Rajandre
 Nature 406, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491
 A:Reference number: AB1775; MUID:20222556
 A:Accession: H81793
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-635 <PAR>
 A:Cross-references: GB:AL162758; GB:AL157959; NID:97380672; PID:CA85416.1; PID:9738
 A:Experimental source: serogroup A, strain 22491
 C:Genetics:
 A:Gene: NMA2205

Query Match 61.8%; Score 34; DB 2; Length 635;
 Best Local Similarity 62.5%; Pred. No. 86;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVF 8
 |||||
 Db 387 HHODLWF 394

RESULT 40
 S51300
 Probable membrane protein YNL311c - yeast (*Saccharomyces cerevisiae*)
 M:Alternate names: hypothetical protein NO376
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
 C:Accession: S51300; S59569; S63292; S63284
 R:Nicaud, J.J.

Submitted to the EMBL Data Library, January 1995
 A:Description: Sequence analysis of a 13.9 Kb fragment of yeast chromosome XIV Ident
 A:Reference number: S51285

A:Accession: S51300
 A:Molecule type: DNA
 A:Residues: 1-763 <NIC>
 A:Cross-references: EMBL:246259; NID:9633655; PID:9633671
 R:Maftah, M.; Nicaud, J.M.; Levesque, H.; Gallardin, C.
 Yeast 11, 1077-1085, 1995
 A:Title: Sequencing analysis of a 24.7 kb fragment of yeast chromosome XIV identifies
 A:Reference number: S59562; MUID:96076632
 A:Accession: S59565
 A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-763 <MAF>

A:Cross-references: EMBL:246259; NID:9633655; PID:CA86384.1; PID:9633671
 R:Maftah, M.; Nicaud, J.M.; Levesque, H.; Gallardin, C.
 Submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63287
 A:Accession: S63292

A:Molecule type: DNA
 A:Residues: 1-763 <MAV>

A:Cross-references: EMBL:271587; NID:91302414; PID:91302415; MIPS:YNL311C
 A:Experimental source: strain 5286C
 R:Maurer, C.T.C.; Urbanus, J.H.M.; Planta, R.J.

Submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63266
 A:Accession: S63284

A:Molecule type: DNA
 A:Residues: 148-763 <MAU>
 A:Cross-references: EMBL:271587; MIPS:YNL311C

A:Experimental source: strain 5286C
 C:Genetics:

A:Map position: 14L
 C:Superfamily: *Saccharomyces cerevisiae* probable membrane protein YNL311c
 C:Keywords: transmembrane protein
 F:64-80/Domain: transmembrane #status predicted <TM>

Query Match 61.8%; Score 34; DB 2; Length 763;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLV 6
|||||
Db 323 HHOKLV 328

RESULT 41

S07137
DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - garden pea chloroplast (fragment)
C:Species: chloroplast Pisum sativum (garden pea)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 18-Jun-1999
C:Accession: S07137
R:Cozens, A.L.; Walker, J.E.
Biochem. J. 236, 453-460, 1986
A:Title: Pea chloroplast DNA encodes homologues of Escherichia coli ribosomal subunit S2
A:Reference number: S07137; MUID:86323089
A:Accession: S07137
A:Molecule type: DNA
A:Residues: 1-1163 <COZ>
A:Cross-references: EMBL:X03912; NID:912137; PIDN:CAA37545.1; PID:9829325
C:Genetics:
A:Gene: rpoC2
A:Genome: chloroplast
C:Superfamily: chloroplast DNA-directed RNA polymerase beta'-2 chain
C:Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 61.8%; Score 34; DB 2; Length 1163;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HHOKLV 9
|||||
Db 1149 HHOKLV 1157

RESULT 42

S51389
ROM2 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein L8039.3; protein YLR371W
C:Species: Saccharomyces cerevisiae
C>Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 05-Nov-1999
C:Accession: S51389
R:Du, Z.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmid 8039.
A:Reference number: S51377
A:Accession: S51389
A:Molecule type: DNA
A:Residues: 1-1356 <DUZ>
A:Cross-references: EMBL:U19103; NID:9609404; PID:9609407; GSPDB:GN00012; MIPS:YLR371W
A:Gene: ROM2; MIPS:YLR371W
A:Map position: 12R
C:Superfamily: CDC24 homology
F:659-846/Domain: CDC24 homology <CD24>

Query Match 61.8%; Score 34; DB 2; Length 1356;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 3; Mismatches 0; Indels 4; Gaps 1;

QY 1 HHOKLV 10
|||||
Db 1131 HHOKLV 1144

RESULT 43

T18961
FAB1 protein homolog VF11C1L.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18961; T26005
R:Lloyd, C.
submitted to the EMBL Data Library, November 1995

A:Reference number: Z19052

A:Accession: T18961

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1375 <WIL>

A:Cross-references: EMBL:Z67879; PIDN:CAA91791.1; GSPDB:GN00028; CESP:VF11C1L.1

A:Experimental source: clone C05E7

R:Mortimore, B.

submitted to the EMBL Data Library, June 1998

A:Reference number: Z20126

A:Accession: T26005

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1375 <WIL>

A:Cross-references: EMBL:AL023817; PIDN:CAA19436.1; GSPDB:GN00028; CESP:VF11C1L.1

A:Experimental source: clone VF11C1L

C:Genetics:

A:Gene: CESP:VF11C1L.1

A:Map position: X

A:Introns: 109/1; 172/2; 198/3; 396/3; 561/3; 592/2; 647/1; 789/2; 859/3; 1104/3; 123

Query Match 61.8%; Score 34; DB 2; Length 1375;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HHOKLV 9
|||||
Db 840 HHOKLV 847

RESULT 44

PN0637
polyketide synthase pksL - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 19-May-1994 #sequence_revision 06-Feb-1995 #text_change 03-Nov-2000
C:Accession: S25021; PN0637; B69679
R:Scotti, C.; Platt, M.; Cuzon, A.; Tognoni, A.; Grandi, G.; Galizzi, A.; Albertin
submitted to the EMBL Data Library, July 1992
A:Description: A Bacillus subtilis large ORF coding for a polypeptide highly similar
A:Reference number: S25021
A:Accession: S25021
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4427 <SCO>
A:Cross-references: EMBL:Z14098; NID:940057; PIDN:CAA78479.1; PID:940058
R:Scotti, C.; Platt, M.; Cuzon, A.; Perant, P.; Tognoni, A.; Grandi, G.; Galizzi, A.
Gene 130, 65-71, 1993
A:Title: A Bacillus subtilis large ORF coding for a polypeptide highly similar to pol
A:Reference number: PN0637; MUID:93345824
A:Accession: PN0637
A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 164-282; 382-850; 926-1115; 1409-1648; 1665-1761; 1876-2344; 2469-2560; 2609-270

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber

C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal

lechi, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M

koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau

Y, M.; Ogawa, K.; Ogilwara, A.; Oudaga, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete

Rieger, M.; Rivolta, C.; Roche, E.; Roche, B.; Rose, M.; Sadleir, Y.; Sato, T.; Scanl

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiya

T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamano, K.; Yasumoto, K.; Yata, K.; Yoshida

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis

A:Reference number: A69580; MUID:98044033

A:Accession: B69679

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-4427 <RUN>

A:Cross-references: GB:299113; GB:AL009126; NID:g2634090; PIDN:CAB13602.1; PID:g2634102
 A:Experimental source: strain 168
 C:Comment: This enzyme is composed of four synthase units. Until comprises beta-ketosynthase, acyl-carrier protein and acyl-carrier protein domains. Unit3 comprises beta-ketosynthase, acyl-carrier protein and acyl-carrier protein domains.
 C:Genetics:
 A:Gene: PKS; pksx
 C:Superfamily: Bacillus subtilis polyketide synthase pksL; 3-oxoacyl-[acyl-carrier-prote
 C:Keywords: acyltransferase; carrier protein
 F:343-758/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>
 F:1410-1591/Domain: short-chain alcohol dehydrogenase homology <SAD1>
 F:1836-2252/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>
 F:2485-2559/Domain: acyl carrier protein homology <ACPI>
 F:2626-2700/Domain: acyl carrier protein homology <ACPI>
 F:2783-3181/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS3>
 F:3576-3774/Domain: short-chain alcohol dehydrogenase homology <SAD2>
 F:3852-3922/Domain: acyl carrier protein homology <ACP3>
 F:3992-4372/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS4>

Query Match 61.8%; Score 34; DB 2; Length 4427;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLV 6
 DB 691 HHOKLV 696

RESULT 45
 S39644
 acetoins utilization protein acub - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 08-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C:Accession: S39644; D69582
 R:Grundv, F.J.; Waters, D.A.; Takova, T.Y.; Henkin, T.M.
 MOL. Microbiol. 10, 259-271, 1993
 A:Title: Identification of genes involved in utilization of acetate and acetoin in Bacti
 A:Reference number: S39641; MUID:95020526
 A:Accession: S39644
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-214 <GRN>
 A:Cross-references: GB:LI17309; NID:9861173; PIDN:AAA68285.1; PID:g3448051
 R:Kunst, F.; Ogatawara, N.; Moser, I.; Albertin, A.M.; Alloni, G.; Azevedo, V.; Berter
 C: Bron, S.; Broillet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabbri, C.; Ferrati, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fuma, S.; Gallizzi, A.; Gallier
 tech, J.; Harwood, C.R.; Hentaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadale, X.; Sato, T.; Scanlon,
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, X.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Sero
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033
 A:Accession: D69582
 A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-214 <KUN>
 A:Cross-references: GB:299119; GB:AL009126; NID:g2635411; PIDN:CAB1948.1; PID:el185843;
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: acub

Query Match 60.0%; Score 33; DB 2; Length 214;
 Best Local Similarity 83.3%; Pred. No. 43;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLV 6
 DB 691 HHOKLV 696

DB 110 HHOKLI 115

RESULT 46
 S41511
 Brn-3a protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Dec-1994 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
 C:Accession: S41511
 R:Thell, T.; McLean-Hunter, S.; Zoernig, M.; Moorey, T.
 Nucleic Acids Res. 21, 5921-5929, 1993
 A:Title: Mouse Brn-3 family of POU transcription factors: a new aminoterminal domain
 A:Reference number: S41511; MUID:94119691
 A:Accession: S41511
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-255 <THE>
 C:Superfamily: unassigned homeobox proteins; homeobox homology; POU domain homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:110-180/Domain: POU domain homology <POU>
 F:199-255/Domain: homeobox homology <HOX>

Query Match 60.0%; Score 33; DB 2; Length 255;
 Best Local Similarity 60.0%; Pred. No. 52;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 HHOKLVFAE 10
 DB 107 HHRELEFAE 116

RESULT 47
 D72217
 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: D72217
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MUID:99287316
 A:Accession: D72217
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-258 <ARN>
 A:Cross-references: GB:AE001812; GB:AE000512; NID:g4982302; PIDN:AD36798.1; PID:g498
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM1733
 C:Superfamily: conserved hypothetical protein HI0072

Query Match 60.0%; Score 33; DB 2; Length 258;
 Best Local Similarity 50.0%; Pred. No. 53;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 HHOKLVFAE 10
 DB 140 HHSSMMFFAD 149

RESULT 48
 A47003
 cytokine receptor family class II protein CRF2-4 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 01-Dec-2000
 C:Accession: A47003; G01418
 R:Rintulla, G.; Gardiner, K.; Uze, G.
 Genomics 16, 366-373, 1993
 A:Title: A new member of the cytokine receptor gene family maps on chromosome 21 at 1
 A:Reference number: A47003; MUID:93300510
 A:Accession: A47003

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-325 <LUT>
 A:Cross-references: GB:Z17227; NID:q393378; PIDN:CAA7893.1; PID:q393379
 R:Lutfalla, G.
 submitted to the EMBL Data Library, April 1994
 A:Reference number: G06935
 A:Accession: G01418
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-123, 'D', 125-268, 'VGME' <LUT>
 A:Cross-references: EMBL:U08988; NID:q571295; PID:q571296
 C:Genetics:
 A:Gene: GDB:CFR4; CRE2-4
 A:Cross-references: GDB:138168; OMIM:123889
 A:Map position: 21q, 21q22.1-21q22.2
 A:Introns: 17/1; 58/2; 111/1; 166/3; 216/1
 C:Keywords: transmembrane, protein

Query Match 60.0%; Score 33; DB 2; Length 325;
 Best Local Similarity 55.6%; Pred. No. 67;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 HHQKLVFFA 9
 |||
 DB 274 HHNTLFFS 282

RESULT 49

T20562
 hypothetical protein F07H5.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T20562
 R:Steward, C.
 submitted to the EMBL Data Library, December 1995
 A:Reference number: Z19292
 A:Accession: T20562
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-334 <WIL>
 A:Cross-references: EMBL:Z68314; PIDN:CAA92663.1; GSPDB:GN00020; CESP:F07H5.2
 A:Experimental source: clone F07H5
 C:Genetics:
 A:Gene: CESP:F07H5.2
 A:Map position: 2
 A:Introns: 72/2; 146/3; 217/1; 280/3

Query Match 60.0%; Score 33; DB 2; Length 334;
 Best Local Similarity 75.0%; Pred. No. 69;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 OKLVEFAE 10
 |||
 DB 195 OKLVEFAE 202

RESULT 50

S32170
 phytoene synthetase - Myxococcus xanthus
 C:Species: Myxococcus xanthus
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 02-Mar-2001
 C:Accession: S32170; S67951
 R:Botella, J.; Murillo, F.; Ruiz-Vazquez, R.
 submitted to the EMBL Data Library, March 1993
 A:Description: Nucleotide and deduced protein sequences of a carotenoid gene cluster in
 A:Reference number: S32168
 A:Accession: S32170
 A:Molecule type: DNA
 A:Residues: 1-336 <BOT>
 A:Cross-references: EMBL:Z21955; NID:q577589; PIDN:CAA9957.1; PID:q288222
 A:Experimental source: strain DK1050
 R:Botella, J.A.; Murillo, F.J.; Ruiz-Vazquez, R.

Eur. J. Biochem. 233, 238-248, 1995
 A>Title: A cluster of structural and regulatory genes for light-induced carotenogenes
 A:Reference number: S67950; MUID:96061955
 A:Accession: S67951
 A:Molecule type: DNA
 A:Residues: 151-175; 185-213 <BOM>
 C:Genetics:
 A:Start codon: GTG
 C:Superfamily: Mycobacterium marinum phytoene synthase

Query Match 60.0%; Score 33; DB 2; Length 336;
 Best Local Similarity 66.7%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 HHQKLVFFA 9
 |||
 DB 23 HHAKSFFFA 31

Search completed: October 29, 2002, 09:24:30
 Job time : 19 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 09:23:27 ; Search time 11 Seconds
(without alignments)
35.200 Million cell updates/sec

Title: US-09-724-842A-27

Perfect score: 55

Sequence: 1 HHQKLVFAE 10

Scoring table: BIOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 105224 seqs, 38719550 residues

105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	57	1 A4_PIG	Q29023 sus scrofa
2	55	100.0	57	1 A4_URMSA	Q29149 ursus marit
3	55	100.0	58	1 A4_CANFA	Q28280 canis faml
4	55	100.0	58	1 A4_RABIT	Q28748 oryctolagus
5	55	100.0	58	1 A4_SHEEP	Q28757 ovis aries
6	55	100.0	59	1 A4_BOVIN	Q28053 bos taurus
7	55	100.0	751	1 A4_SAISC	Q95241 salmtr sci
8	55	100.0	770	1 A4_HUMAN	P05067 homo sapien
9	47	85.5	770	1 A4_MOUSE	P13023 mus musculu
10	47	85.5	770	1 A4_RAT	P08592 rattus norv
11	39	70.9	699	1 MALQ_HAEIN	P45176 haemophilus
12	38	69.1	549	1 G6PI_ECOLI	P15373 escherichia
13	38	69.1	550	1 G6PI_VIBCH	Q9KUY4 vibrio chol
14	36	65.5	109	1 SAS_PIG	Q29257 sus scrofa
15	36	65.5	204	1 TNE6_HUMAN	Q98857 homo sapien
16	36	65.5	210	1 SAS_HUMAN	Q12999 homo sapien
17	35	63.6	549	1 G6PI_BOVAT	P57636 bucheira ap
18	35	63.6	549	1 G6PI_PASMU	Q96312 pasteurella
19	35	63.6	849	1 RSG2_HUMAN	Q15283 homo sapien
20	35	63.6	2347	1 KROS_HUMAN	P08922 homo sapien
21	34	61.8	124	1 SLP_BACSU	P39910 bacillus su
22	34	61.8	763	1 YNS1_YEAST	P42843 saccharomyc
23	34	61.8	1163	1 RPOD_PEA	P12227 pisum sativ
24	34	61.8	1356	1 ROM2_YEAST	P51862 saccharomyc
25	34	61.8	2715	1 TRX2_HUMAN	Q9UNM6 homo sapien
26	34	61.8	4427	1 PKSL_BACSU	Q05470 bacillus su
27	33	60.0	214	1 ACUB_BACSU	P39066 bacillus su
28	33	60.0	258	1 PPKK_THEMA	Q9X255 thermotoga
29	33	60.0	325	1 I10S_HUMAN	Q08334 homo sapien
30	33	60.0	496	1 C7D9_SOYBN	O081971 glycine max
31	33	60.0	549	1 G6PI_HAEIN	P44312 haemophilus
32	33	60.0	564	1 SYT_MYCCE	P47615 mycoplasma
33	33	60.0	2150	1 SDC3_CABEL	P34706 caenorhabdi

34	32	58.2	167	1	G6PI_KLEOX	P77877 klebsiella
35	32	58.2	178	1	CALC_MOUSE	Q63811 mus musculu
36	32	58.2	321	1	CYF_GUITH	Q78494 guillardi
37	32	58.2	380	1	FD3E_SOYBN	P48625 glycine max
38	32	58.2	481	1	LBP_HUMAN	P18428 homo sapien
39	32	58.2	492	1	CPBL_MOUSE	O55071 mus musculu
40	32	58.2	495	1	MORC_MOUSE	Q92458 rickettsia
41	32	58.2	501	1	ACHB_MOUSE	P09690 mus musculu
42	32	58.2	517	1	ACHB_HUMAN	P07510 homo sapien
43	32	58.2	519	1	ACHB_BOVIN	P13535 bos taurus
44	32	58.2	519	1	ACHB_MOUSE	P04760 mus musculu
45	32	58.2	519	1	ACHB_RAT	P18916 rattus norv
46	32	58.2	557	1	PRXY_ASCNO	P81701 ascophyllum
47	32	58.2	616	1	YAMG_SCHPO	Q10190 schizosach
48	32	58.2	734	1	GLGB_AGRTV	P52979 agrobacteri
49	32	58.2	808	1	PLD_PIMBR	O04883 plimpinella
50	32	58.2	808	1	PLD_RICCO	Q41142 ricinus com

ALIGNMENTS

RESULT 1
A4_PIG
ID A4_PIG
AC Q29023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-Ap) (A-beta)] (Fragment).
GN A4_P.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(C) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
CC -----
DR EMBL, X56127; CA439592.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR01868; A4_APP.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neutone; Transmembrane.
FT NON_TER 1
FT CHAIN 6 48
FT DOMAIN <1 33 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT NON_TER 57 57
FT SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;
Query Match 100.0%; Score 55; DB 1; Length 57;

Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVEFAE 10
DB 18 HHOKLVEFAE 27

RESULT 2

AA_URMA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalassios maritimus).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
RT Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G/O (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

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CC
CC EMBL: X56128; CA39593.1; -
CC HSSP: P05067; 1AHL.
CC InterPro: IPR001868; A4_APP.
CC PROSITE: PS00319; A4_EXTRA; PARTIAL.
CC PROSITE: PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurope; Transmembrane.
FT CHAIN 1 48 BETA-AMYLOID PROTEIN (POTENTIAL);
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL);
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 100.0%; Score 55; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVEFAE 10
DB 18 HHOKLVEFAE 27

RESULT 3

AA_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
RT Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G/O (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

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CC
CC EMBL: X56125; CA39590.1; -
CC HSSP: P05067; 1BA4.
CC InterPro: IPR001868; A4_APP.
CC PROSITE: PS00319; A4_EXTRA; PARTIAL.
CC PROSITE: PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurope; Transmembrane.
FT CHAIN 1 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D48A2E12DFA CRC64;

Query Match 100.0%; Score 55; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVEFAE 10
DB 19 HHOKLVEFAE 28

RESULT 4

AA_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid

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RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis".
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56129; CAA39594.1; -.
CC HSSP; P05067; 1BA4.
CC InterPro: IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC NON_TER 1 1
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 34 57 POTENTIAL.
CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
CC NON_TER 58 58
CC SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 55; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. NO. 0.0002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
   |||||
Db 18 HHOKLVFAE 27

RESULT 5
A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [contains: Beta-amyloid
DE protein (Beta-Ap) (A-beta)] (Fragment).
GN APP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56124; CAA39589.1; -.
CC EMBL; X56126; CAA39591.1; -.
CC HSSP; P05067; 1BA4.
CC InterPro: IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
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CC -----
CC EMBL; X56120; CAA39595.1; -.
CC HSSP; P05067; 1AM1.
CC InterPro: IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
CC NON_TER 1 1
CC CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
CC DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 34 57 POTENTIAL.
CC DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
CC NON_TER 58 58
CC SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 100.0%; Score 55; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. NO. 0.0002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
   |||||
Db 18 HHOKLVFAE 27

RESULT 6
A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-Ap) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL; X56124; CAA39589.1; -.
CC EMBL; X56126; CAA39591.1; -.
CC HSSP; P05067; 1BA4.
CC InterPro: IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
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FT  NON_TER      1      1
FT  CHAIN         7      49      BETA-AMYLOID PROTEIN (POTENTIAL).
FT  DOMAIN        <1     34      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM      35     58      POTENTIAL.
FT  DOMAIN        59     >59      CYTOPLASMIC (POTENTIAL).
FT  NON_TER      59     59
SQ  SEQUENCE      59 AA; 6414 MW; F43469D48A2E12D CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 1; Length 59;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 HHOKLVFAAE 10
    |||||
DB  19 HHOKLVFAAE 28

RESULT 7
A4_SAISC STANDARD; PRT; 751 AA.
AC 095241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [contains: Beta-
DE amyloid protein (Beta-ApP) (A-beta)].
GN APp.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
MEDLINE=96108492; PubMed=8532114;
Levy E., Amornit A., Frangione B., Walker L.C.;
"Beta-amyloid precursor protein gene in squirrel monkeys with
RT cerebral amyloid angiopathy.";
RL Neurobiol. Aging 16:805-808(1995).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPPI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL: S81024; AADI4347.1; -
DR HSP: P05067; IAAp.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPPI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPPI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KT; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPPI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPPI_KUNITZ_2; 1.

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KM Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
KM Signal; Serine protease inhibitor.
FT SIGNAL         1      17
FT CHAIN         18     751      BY SIMILARITY.
FT CHAIN         653     751      A4 PROTEIN.
FT DOMAIN        695     695      BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM      18     680      EXTRACELLULAR (POTENTIAL).
FT TRANSMEM      681     704      POTENTIAL.
FT DOMAIN        705     751      CYTOPLASMIC (POTENTIAL).
FT DOMAIN        287     345      BPPI/KUNITZ INHIBITOR.
FT SITE          740     743      CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE      301     302      REACTIVE BOND.
FT DISULFID      291     341      BY SIMILARITY.
FT DISULFID      300     324      BY SIMILARITY.
FT DISULFID      316     337      BY SIMILARITY.
FT CARBOHYD      523     523      N-LINKED (GLCNAC...) (PROBABLE).
FT CARBOHYD      552     552      N-LINKED (GLCNAC...) (PROBABLE).
SQ  SEQUENCE      751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 1; Length 751;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1 HHOKLVFAAE 10
    |||||
DB  665 HHOKLVFAAE 674

RESULT 8
A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)
DE (PN-II) (APPI) [Contains: Beta-amyloid protein (Beta-ApP) (A-beta)].
GN APP OR A4 OR CVAP OR ADL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
MEDLINE=87144572; PubMed=2881207;
Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor.";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=8812639; PubMed=2893289;
Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors.";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC MEDLINE=89128427; PubMed=2783775;
Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons.";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A.
RC MEDLINE=97263807; PubMed=9108164;
Hattori M., Tsukahara F., Furuhara Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for

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RT sequencing of a 300 kb region of human APP locus.";
 RL Nucleic Acids Res. 25:1802-1808(1997).
 RN
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE-88122640; PubMed-2893290;
 RA Tanzi R.E., McClatchey A.I., Lampertl E.D., Villa-Komaroff L.,
 RA Gusella J.F., Nave R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RT mRNA associated with Alzheimer's disease.";
 RL Nature 331:528-530(1988).
 RN
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE-88122641; PubMed-2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RT protease inhibitory activity.";
 RL Nature 331:530-532(1988).
 RN
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE-87231971; PubMed-3035574;
 RA Rodakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RT cerebrovascular and the neuritic plaque amyloid peptides.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 RN
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE-88124954; PubMed-2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RT disease brain: coding and noncoding regions of the fetal precursor
 RT mRNA are expressed in the cortex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 RN
 RP SEQUENCE OF 672-681.
 RX MEDLINE-88035004; PubMed-3312495;
 RA Pardridge W.M., Winters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiotensin of Alzheimer's disease: amino acid composition
 RT and partial sequence of a 4,200-dalton peptide isolated from cortical
 RT microvessels.";
 RL J. Neurochem. 49:1394-1401(1987).
 RN
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE-90236318; PubMed-2110105;
 RA Yoshikai S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RT gene.";
 RL Gene 87:257-263(1990).
 RN
 RP SEQUENCE OF 1-10 FROM N.A.
 RX MEDLINE-89016647; PubMed-3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABP)
 RT encodes a 99-kDa polypeptide.";
 RL Nucleic Acids Res. 16:9351-9351(1988).
 RN
 RP SEQUENCE OF 18-50.
 RX MEDLINE-87250462; PubMed-3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RL J. Biol. Chem. 262:8508-8514(1987).
 RN
 RP IDENTITY OF APP WITH NEXIN-II.
 RX MEDLINE-8934866; PubMed-2506449;
 RA Oltersdorf T., Frits L.C., Schenk D.B., Lieberburg I.,
 RA Johnson Wood K.L., Beattie E.C., Ward P.J., Blachere R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II.";
 RL Nature 341:144-147(1989).
 RN
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE-90211252; PubMed-1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RT disease amyloid protein precursor.";
 RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
 RN
 RP COMPLEX WITH G(O).
 RX MEDLINE-9318965; PubMed-8446172;
 RA Nishimoto I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RT protein G(O).";
 RL Nature 362:75-79(1993).
 RN
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE-99215582; PubMed-10201399;
 RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RT Alzheimer amyloid precursor protein.";
 RL Nat. Struct. Biol. 6:327-331(1999).
 RN
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE-91104913; PubMed-2125487;
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RT Alzheimer's amyloid beta-protein precursor.";
 RL Biochemistry 29:10018-10022(1990).
 RN
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE-92031488; PubMed-1718421;
 RA Heald S.L., Tilton R.F., Jr., Hammond L.S., Lee A., Bayney R.M.,
 RA Kamarcik M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Untebeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RT precursor protein.";
 RL Biochemistry 30:10467-10478(1991).
 RN
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE-94281210; PubMed-7516706;
 RA Talafoos J., Marcinkowski R.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RL Biochemistry 33:7788-7796(1994).
 RN
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE-97128622; PubMed-8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RT membrane-mimicking environment.";
 RL Biochemistry 35:16094-16104(1996).
 RN
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE-98359783; PubMed-9693002;
 RA Coles M., Blockell W., Watson A.A., Fairlie D.P., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscelle
 RT environment. Is the membrane-spanning domain where we think it is?";
 RL Biochemistry 37:11064-11077(1998).
 RN
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE-20400066; PubMed-10940222;
 RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site.";
 RL J. Struct. Biol. 130:142-152(2000).
 RN
 RP STRUCTURE BY NMR OF 681-706.
 RX MEDLINE-20400065; PubMed-10940221;
 RA Zhang S., Iwata K., Lachemann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RT the Kunitz domain is protease nexin-II.";
 RL Nature 341:144-147(1989).
 RN

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RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
RT water."
RL J. Struct. Biol. 130:130-141(2000).
RN [24]
RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
RX MEDLINE-8296437; PubMed-2900137;
RA Dyrks T., Weidemann A., Muthaup G., Salbaum J.M., Lemaire H.-G.,
RA Kang U., Mueller-Hill B., Masters C.L., Beyreuther K.;
RT "Identification, transmembrane orientation and biogenesis of the
RT amyloid A4 precursor of Alzheimer's disease."
Query Match 100.0%; Score 55; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HXORLVEAFE 10
Db 684 HXORLVEAFE 693
RESULT 9
A4_MOUSE STANDARD; PRT; 770 AA.
ID A4_MOUSE
AC p12023;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP STRAIN-BALB/C; TISSUE-Brain;
RX MEDLINE-92096458; PubMed-1756177;
RA de Strooper B., van Leuven F., Van den Bergh H.;
RT "The amyloid beta protein precursor or protease nexin II from mouse
RL Biochim. Biophys. Acta 1129:141-143(1991).
[2]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RX TISSUE-Brain;
RX MEDLINE-88106489; PubMed-3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
[3]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE OF 289-364 FROM N.A.
RX STRAIN-CD-1; TISSUE-Placenta;
RX MEDLINE-89345111; PubMed-2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RL Precursor of Mus domesticus."
RT Nucleic Acids Res. 17:5396-5396(1989).
[5]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE-9209998; PubMed-1555768;
RA Isumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RT Alzheimer's disease amyloid precursor-encoding gene in mouse."
RL Gene 112:189-195(1992).
[6]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RX TISSUE-Brain, and Kidney;

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RX MEDLINE-89149813; PubMed-2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RT for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor."
RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE), ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC LIVER.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC -----
DR EMBL; X59379; -; NOT_ANNOTATED_CDS.
DR EMBL; M18373; AAA37139.1; -;
DR EMBL; X15210; CAA33280.1; -;
DR EMBL; D10603; BAA01456.1; -;
DR EMBL; M24397; AAA39929.1; -;
DR PIR; A27485; A27485.
DR PIR; S04855; S04855.
DR PIR; S19727; S19727.
DR HSP; P05067; IQCM.
DR MGD; MGI:88059; App.
DR InterPro; IPR001868; A4 APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT FT
FT CHAIN 1 770
FT FT
FT FT
FT DOMAIN 18 699
FT TRANSMEM 700 723
FT DOMAIN 724 770
FT DOMAIN 673 715
FT DOMAIN 287 345
FT SITE 759 762
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 542 542
FT CARBOHYD 571 571
FT VARSPPLIC 289 289
FT VARSPPLIC 290 364
FT VARSPPLIC 346 380
SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CA7A CRC64;
Query Match 85.5%; Score 47; DB 1; Length 770;

```

Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVEFAE 10
DB 685 HOKLVEFAE 693

RESULT 10

ID	NAME	STANDARD	PRT	770 AA
AC	A4_RAT			
AC	P08592;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Alzheimer's disease amyloid A4 protein homolog precursor			
DE	(Amyloidogenic glycoprotein) (AG).			
GN	APP.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE OF 1-289 AND 365-770 FROM N.A.			
RC	TISSUE=Brain;			
RC	MEDLINE=88312583; PubMed=2900758;			
RX	Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,			
RA	Seeburg P.H.;			
RT	"Alzheimer's disease amyloidogenic glycoprotein: expression pattern			
RT	in rat brain suggests a role in cell contact.";			
RL	EMBO J. 7:1365-1370(1988).			
RN	[2]			
RP	SEQUENCE OF 289-364 FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=89183625; PubMed=2648331;			
RA	Kang J., Mueller-Hill B.;			
RT	"The sequence of the two extra exons in rat preA4.";			
RL	Nucleic Acids Res. 17:2130-2130(1989).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),			
CC	APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE			
CC	SPlicing.			
CC	-1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION			
CC	WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC			
CC	RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE			
CC	NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF			
CC	PHOSPHORYLATION (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE APP FAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.			
CC	-----			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X07648; CAA30488.1;			
DR	EMBL; X14066; CAA32229.1;			
DR	PIR; S00550; S00550.			
DR	PIR; S03607; S03607.			
DR	HSSP; P05067; 1AAP.			
DR	InterPro: IPR001868; A4_APP.			
DR	InterPro: IPR002223; Kunitz_BPTI.			
DR	Pfam: PF02177; A4_EXTRA.1.			
DR	Pfam: PF00014; Kunitz_BPTI.1.			
DR	PRINTS; PR00203; AMYLOIDA.			
DR	PRINTS; PR00753; BASICPTASE.			
DR	SMART; SM00006; A4_EXTRA.1.			
DR	SMART; SM00131; KU.1.			
DR	PROSITE; PS00319; A4_EXTRA.1.			
DR	PROSITE; PS00320; A4_INTRA.1.			

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
KM Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KM Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 1 770
FT DOMAIN 18 699
FT TRANSMEM 700 723
FT DOMAIN 724 770
FT DOMAIN 673 715
FT SITE 287 715
FT DISULFID 291 341
FT DISULFID 300 324
FT DISULFID 316 337
FT CARBOHYD 542 542
FT CARBOHYD 571 571
FT VARSPPLIC 289 289
FT VARSPPLIC 290 364
SQ SEQUENCE 770 AA; 86704 MW; C26C9D6BBD292A7 CRC64;

Query Match
Best Local Similarity 85.5%; Score 47; DB 1; Length 770;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVEFAE 10
DB 685 HOKLVEFAE 693

RESULT 11

ID	NAME	STANDARD	PRT	699 AA
AC	P45176;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	4-alpha-glucanotransferase (EC 2.4.1.25) (Amylomalase)			
DE	(Disproportionating enzyme) (D-enzyme).			
GN	MALO OR Hii356.			
OS	Haemophilus influenzae.			
OC	Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;			
OC	Haemophilus.			
OX	NCBI_TaxID=727;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=RD / KW20 / ATCC 51907;			
RX	MEDLINE=95350630; PubMed=7542800;			
RA	Kerlavange A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,			
RA	McKenny K., Sutton G., Fitchugh W., Fields C.A., Gocayne J.D.,			
RA	Scott J.D., Shirley R., Liu L.-T., Glodex A., Kelley J.M.,			
RA	Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,			
RA	Usterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,			
RA	Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,			
RA	Guenem C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,			
RA	Venter J.C.;			
RT	"Whole-genome random sequencing and assembly of Haemophilus			
RT	influenzae Rd.";			
RL	Science 269:496-512(1995).			
CC	-1- CATALYTIC ACTIVITY: Transfers a segment of a (1,4)-alpha-D-glucan			
CC	to a new 4-position in an acceptor, which may be glucose or (1,4)-			
CC	alpha-D-glucan.			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).			
CC	-1- SIMILARITY: BELONGS TO THE DISPROPORTIONATING ENZYME FAMILY.			
CC	-----			
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CC -----
DR EMBL: U32815; AAC23003.1;
DR TIGR: H1356;
DR InterPro: IPR003385; 4A-glucanotrans.
DR Pfam: PF02446; 4A-glucanotrans; 1.
KW Transferrase; Glycosyltransferase; Carbohydrate metabolism;
KM Complete proteome.
SQ SEQUENCE 699 AA; 80251 MW; 80D6E1D51EC2E1E9 CRC64;

Query Match
Best Local Similarity 66.7%; Score 39; DB 1; Length 699;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HHOKLVFA 9
DB 349 HHKIOFFA 357

RESULT 12
G6PI_ECOLI STANDARD; PRT; 549 AA.
ID G6PI_ECOLI
AC P11537;
DT 01-OCT-1989 (Rel. 12, Created)
DI 01-MAR-2002 (Rel. 41, Last sequence update)
DI 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
GN isomerase) (Pgi) (Phosphohexose isomerase) (PHI).
OS Escherichia coli.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JM101;
RX MEDLINE-89364675; PubMed-2549364;
RT Fromman B.E., Tait R.C., Gottlieb L.D.;
RT "Isolation and characterization of the phosphoglucose isomerase gene
RT from Escherichia coli."
RL Mol. Gen. Genet. 217:126-131(1989).
RN [2]
RP SEQUENCE FROM N.A., AND PHYLOGENETIC STUDY.
RC STRAIN-XL1 BLUE 2;
RX MEDLINE-92277670; PubMed-1593646;
RT Smith M.W., Doolittle R.F.;
RT "Anomalous phylogeny involving the enzyme glucose-6-phosphate
RT isomerase."
RL J. Mol. Evol. 34:544-545(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-94089392; PubMed-8265357;
RT Blatter F.R., Burland V.D., Plunkett G. III, Sofia H.J.;
RA Daniels D.L.;
RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
RT region from 89.2 to 92.8 minutes."
RL Nucleic Acids Res. 21:5408-5417(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE-21074935; PubMed-11206551;
RA Pena N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lin A., Dimalanta E.T., Potamousteris K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blatter F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.

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RC STRAIN-O157:H7 / RIMD 0509952;
RX MEDLINE-21156231; PubMed-11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han S.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate -> D-fructose 6-
CC phosphate.
CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC -----
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CC -----
DR EMBL: X15196; CAA33268.1;
DR EMBL: U00006; AAC43119.1;
DR EMBL: AE000476; AAC76995.1;
DR EMBL: AE005635; AAG59224.1;
DR EMBL: AP002568; BAB38431.1;
DR PIR: J50142; NUCC.
DR Ecogene: EG10702; pgl.
DR InterPro: IPR001672; G6P_Isomerase.
DR Pfam: PF00342; PGI; 1.
DR PRINTS: PR00662; G6PISOMERASE.
DR PROSITE: PS00765; P-GLUCOSE-ISOMERASE_1; 1.
DR PROSITE: PS00174; P-GLUCOSE-ISOMERASE_2; 1.
KW Isomerase; Glucosyltransferase; Glycolysis; Complete proteome.
FT ACT_SITE 386 BY SIMILARITY.
FT ACT_SITE 514 BY SIMILARITY.
FT CONFLICT 317 L -> V (IN REF. 1 AND 2).
SQ SEQUENCE 549 AA; 61529 MW; 74AEDB670A068A01 CRC64;

Query Match
Best Local Similarity 69.1%; Score 38; DB 1; Length 549;
Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 HHOKLV -PFAE 10
DB 416 HHOKLISNFFAQ 427

RESULT 13
G6PI_VIBCH STANDARD; PRT; 550 AA.
ID G6PI_VIBCH
AC Q9K0Y4;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DI 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (Pgi) (Phosphohexose isomerase) (PHI).
GN Pgi OR VC0374.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EL TOR N16961 / SEROTYPE O1;
RX MEDLINE-20406833; PubMed-10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ernolava M.D., Vamathevan J., Bess S., Qin H., Dragoti I., Sellers P.,
RA McDonald L., Uitterback T., Fleischmann R.D., Nierman W.C., White O.,

```

RA Salberg S.L., Smuth H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae";
 RL Nature 406:477-483(2000).
 CC -1- CATALYTIC ACTIVITY: GLUCOSE 6-PHOSPHATE - FRUCTOSE 6-PHOSPHATE.
 CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE004125; AAF93547.1; -
 DR TIGR: VC0374; -
 DR InterPro: IPR001672; G6P_Isomerase.
 DR Pfam: PF00342; PGI: 1
 DR PRINTS: PR00662; G6PISOMERASE.
 DR PROSITE: PS00765; P-GLUCOSE-ISOMERASE_1; 1.
 DR PROSITE: PS00174; P-GLUCOSE-ISOMERASE_2; 1.
 DR Isomerase; Glucosyltransferase; Glycolysis; Complete proteome.
 FT ACT SITE 387 387
 FT ACT SITE 515 515 BY SIMILARITY.
 FT SITE 515 515
 SQ SEQUENCE 550 AA; 60690 MW; 5E38B0421C3A1B16 CRC64;
 Query Match 69.1%; Score 38; DB 1; Length 550;
 Best Local Similarity 66.7%; Pred. No. 4.7;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;
 QY 1 HHOKLV--FFAE 10
 Db 417 HHOKLSNFFAQ 428
 RESULT 14
 SAS_PIG STANDARD; PRT; 109 AA.
 ID SAS_PIG
 AC Q29257;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Sarcosin amplified sequence (fragment).
 GN SAS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Small intestine;
 RX MEDLINE=96327607; PubMed=8672129;
 RA Winteroe A.K., Fredholm M., Davies W.;
 RT "Evaluation and characterization of a porcine small intestine CDNA
 RT library: analysis of 839 clones";
 RL Mamm. Genome 7:509-517(1996).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
 DR InterPro: IPR000301; Transmem_4.
 DR Pfam: PF00335; Transmembrane4; 1.
 DR PRINTS: PR00259; TMFOUR.
 KW Glycoprotein; Transmembrane.
 FT DOMAIN 1 12
 FT TRANSMEM 13 33 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 34 44 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 45 65 POTENTIAL.
 FT DOMAIN 66 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 73 93 POTENTIAL.
 FT DOMAIN 94 >109 EXTRACELLULAR (POTENTIAL).

FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11291 MW; 5CC5EAB8B7F152B1 CRC64;
 Query Match 65.5%; Score 36; DB 1; Length 109;
 Best Local Similarity 75.0%; Pred. No. 2.2;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HHOKLVFF 8
 Db 70 HHQVLLFF 77
 RESULT 15
 TNE6_HUMAN STANDARD; PRT; 204 AA.
 ID TNE6_HUMAN
 AC 095857;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tetraspan NET-6.
 GN NET6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rubinstein E., Serru V., Dessen P., Bouchet C.;
 RT "New tetraspans identified in the EST database";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=pituitary;
 RX MEDLINE=20402571; PubMed=10931946;
 RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
 RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,
 RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,
 RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,
 RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
 RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal
 RT axis and full-length cDNA cloning";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF120265; AAD17294.1; -
 DR EMBL: AF100759; AAD43023.1; -
 DR InterPro: IPR000301; Transmem_4.
 DR Pfam: PF00335; Transmembrane4; 1.
 DR PRINTS: PR00259; TMFOUR.
 DR PROSITE: PS00421; TM4_1; FALSE_NEG.
 KW Glycoprotein; Transmembrane.
 FT DOMAIN 1 19
 FT TRANSMEM 20 40 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 41 44 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 45 65 POTENTIAL.
 FT DOMAIN 66 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 73 93 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 94 167 POTENTIAL.
 FT TRANSMEM 168 188 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 189 204 POTENTIAL.
 FT CARBOHYD 113 113 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 204 AA; 22147 MW; 5928646BCD83CD06 CRC64;

Query Match 65.5% Score 36; DB 1; Length 204;
 Best Local Similarity 75.0%; Pred. No. 4.2;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVFF 8
 ||| |||
 Db 70 HHQVLEFF 77

RESULT 16
 ID SAS_HUMAN STANDARD; PRT: 210 AA.
 AC Q12999; 000577;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Sarcosin amplified sequence.
 GN SAS.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCB1; TaxID:9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Osteosarcoma;
 RA MEDLINE-94181273; PubMed-8134123;
 RA Jankowski S.A., Mitchell D.S., Smith S.H., Trent J.M., Meltzer P.S.;
 RT "SAS, a gene amplified in human sarcomas, encodes a new member of the
 transmembrane 4 superfamily of proteins.";
 RL Oncogene 9:1205-1211(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-97336055; PubMed-9192850;
 RA Elieghoun A.G., Kizman D.B., Wang Z., Hofmann T.A., Roe B.A.,
 RA Meltzer P.S.;
 RT "Transcript mapping in a 46-kb sequenced region at the core of 12q13.3
 amplification in human cancers.";
 RL Genomics 42:295-301(1997).
 RN [3]
 RP REVISIONS TO 76-77 AND 205-210.
 RA Roe B.A.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Prostate;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE TETRASPANIN (TM4SF) FAMILY.
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FT DOMAIN 94 173 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 174 194 POTENTIAL.
 FT DOMAIN 195 210 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 100 100 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 109 109 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 117 117 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 134 134 N-LINKED (GLCNAc. . .) (POTENTIAL).
 SO SEQUENCE 210 AA; 23053 MW; 8A1F8C5319755E CRC64;

Query Match 65.5% Score 36; DB 1; Length 210;
 Best Local Similarity 75.0%; Pred. No. 4.3;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVFF 8
 ||| |||
 Db 70 HHQVLEFF 77

RESULT 17
 ID G6PI_BUCAL STANDARD; PRT: 549 AA.
 AC P57636;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
 isomerase) (PGI) (Phosphohexose isomerase) (PHI).
 GN PGI OR BU573.
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
 CC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 NC NCB1; TaxID:118099;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TOKYO 1998;
 RX MEDLINE-20445173; PubMed-1093077;
 RA Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 Buchnera sp. APS.";
 RL Nature 407:81-86(2000).
 CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
 phosphate.
 CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
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DR EMBL; AP001119; BABJ3263.1;
 DR InterPro: IPR001672; G6P_Isomerase.
 DR Pfam: PF00342; PGI; 1.
 DR PRINTS: PR00662; G6PISOMERASE.
 DR PROSITE: PS00765; P-GLUCOSE-ISOMERASE 1; 1.
 DR PROSITE: PS00174; P-GLUCOSE-ISOMERASE 2; 1.
 KW ACT_SITE; Glucosyltransferase; Glycolysis; Complete proteome.
 FT ACT_SITE 386 386
 FT ACT_SITE 514 514
 SO SEQUENCE 549 AA; 63435 MW; 8D547CE08382244 CRC64;

Query Match 63.6% Score 35; DB 1; Length 549;
 Best Local Similarity 58.3%; Pred. No. 18;
 Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

OY 1 HHOKLVFF-PEAE 10
 ||| |||
 Db 416 HHKLSNFFAQ 427

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RESULT 18
G6PI_PASMU STANDARD; PRT: 549 AA.
AC 09CNL2;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
  isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN PGI OR PM0416.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
  Pasteurella.
OX NCBI_Taxid=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida pm70."
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- CATABOLIC ACTIVITY: GLUCOSE 6-PHOSPHATE -> FRUCTOSE 6-PHOSPHATE.
CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (By similarity).
CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC -----
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CC -----
DR EMBL: AE006077; AAK02500.1;
DR InterPro: IPR001672; G6P_Isomerase.
DR Pfam: PF00342; PGI: 1.
DR PRINTS: PRO0662; G6PISOMERASE.
DR PROSITE: PS00765; P_GLUCOSE_ISOMERASE.1; 1.
DR PROSITE: PS00174; P_GLUCOSE_ISOMERASE.2; 1.
DR KMW isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT ACT SITE 387
FT ACT SITE 387 BY SIMILARITY.
FT ACT SITE 515 515 BY SIMILARITY.
SO SEQUENCE 549 AA; 61437 MW; E6E856927B93283 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 549;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 3; Mismatches 0; Indels 2; Gaps 1;

QY 1 HHOKLV--FFAE 10
DB 417 HHKLLSNFFAQ 428

RESULT 19
RSG2_HUMAN STANDARD; PRT: 849 AA.
AC 015283; Q15284; O00695; Q99577; Q92594; Q9UEQ2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Ras GTPase-activating protein 2 (GAP1m).
GN RAS2 OR RASGAP OR GAP1m.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97074668; PubMed=8917095;
RA Kobayashi M., Masui T., Kusuda J., Kameoka Y., Hashimoto K.,
  Iwashita S.;

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RT "Human rasGTPase-activating protein (human counterpart of GAP1m):
RT sequence of the cDNA, primary structure of the protein, production and
RT chromosomal localization."
RL Gene 175:173-177(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97001173; PubMed=8812506;
RA Li S., Satoh H., Watanabe T., Nakamura S., Hattori S.;
RT "cDNA cloning and chromosomal mapping of a novel human GAP (GAP1m), a
RT GTPase-activating protein of Ras."
RL Genomics 35:625-627(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=98044291; PubMed=9382842;
RA Lockyer P.J., Bottomley J.R., Reynolds J.S., McNulty T.J.,
RA Venkateswarlu K., Potter B.V.L., Dempsey C.E., Cullen P.J.;
RT "Distinct subcellular localisations of the putative inositol 1,3,4,5-
RT tetrakisphosphate receptors GAP1(IP4BP) and GAP1m result from the
RL Curr. Biol. 7:1007-1010(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Lockyer P.J.;
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: INHIBITORY REGULATOR OF THE RAS-CYCIC AMP PATHWAY.
CC BINDS INOSITOL TETRAPHOSPHATE (IP4).
CC -1- SUBCELLULAR LOCATION: PERINUCLEAR AND CYTOPLASMIC.
CC -1- SIMILARITY: CONTAINS 2 C2 DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BTK DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RAS-GAP DOMAIN.
CC -----
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CC -----
DR EMBL: D78155; BA11230.1;
DR EMBL: D78156; BA11231.1;
DR EMBL: D82880; BA11621.1;
DR EMBL: D82881; BA11622.1;
DR EMBL: AF115573; AAD09821.1;
DR HSP: P21707; IRSY.
DR MIM: 601589;
DR InterPro: IPR001562; BTK.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001849; PH.
DR InterPro: IPR001936; RASGAP.
DR Pfam: PF00779; BTK; 1.
DR Pfam: PF00168; C2; 2.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00616; RASGAP; 1.
DR PRINTS: PRO0402; TECBTKDOMAIN.
DR SMART: SM00107; BTK; 1.
DR SMART: SM00239; C2; 2.
DR SMART: SM00233; PH; 1.
DR SMART: SM00323; RASGAP; 1.
DR PROSITE: PS50003; PH_DOMAIN; 1.
DR PROSITE: PS00489; C2_DOMAIN; 1. FALSE_NEG.
DR PROSITE: PS50004; C2_DOMAIN; 2.
DR PROSITE: PS00509; RAS_GTPASE_ACTIV_1; FALSE_NEG.
DR PROSITE: PS50018; RAS_GTPASE_ACTIV_2; 1.
DR GTPase activation; Repeat.
FT DOMAIN 25 122 C2 DOMAIN 1.
FT DOMAIN 166 273 C2 DOMAIN 2.
FT DOMAIN 356 550 PH.
FT DOMAIN 604 705 PH.

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FT DOMAIN 707 743 BTR.
 FT DOMAIN 1 26 ALA-RICH.
 FT CONFLICT 216 216 T -> A (IN REF. 1).
 FT CONFLICT 645 645 G -> GS (IN REF. 1).
 FT CONFLICT 645 645 G -> EFIE (IN REF. 2).
 SQ SEQUENCE 849 AA: 96526 MW: A4B491DFF5C4CB76 CRC64;
 Query Match 63.6%; Score 35; DB 1; Length 849;
 Best Local Similarity 77.8%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HHOKLVFEFA 9
 Db 370 HHDKLVFEFA 378
 RESULT 20
 ID KROS_HUMAN STANDARD; PRT; 2347 AA.
 AC P08922; Q15368;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase ROS precursor (BC 2.7.1.112).
 GN ROS1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RA Birmelmeier C., O'Neill K., Riggs M., Wigler M.;
 RT "Characterization of ROS1 cDNA from a human glioblastoma cell line,"
 RL Proc. Natl. Acad. Sci. U.S.A. 87:4799-4803(1990).
 RN [2]
 RA Matsushime H., Wang L.-H., Shibuya M.;
 RT "Human c-ros-1 gene homologous to the v-ros sequence of UR2 sarcoma
 RL virus encodes for a transmembrane receptorlike molecule,"
 RL Mol. Cell. Biol. 6:3000-3004(1986).
 RN [3]
 RA Birmelmeier C., Birnbaum D., Matthes G., Fasano O., Wigler M.;
 RT "Characterization of an activated human ros gene,"
 RL Mol. Cell. Biol. 6:3109-3116(1986).
 CC -1- FUNCTION: THIS IS A PROBABLY A CELL GROWTH OR DIFFERENTIATION
 CC FACTOR RECEPTOR WITH A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
 CC PROTEIN KINASES. SEVENTEEN SUBFAMILY.
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 DR EMBL; M34353; AAA60277.1; -
 DR EMBL; M13599; AAA60277.1; -
 DR EMBL; M13368; AAA60277.1; JOINED.
 DR EMBL; M13591; AAA60277.1; JOINED.
 DR EMBL; M13592; AAA60277.1; JOINED.
 DR EMBL; M13593; AAA60277.1; JOINED.
 DR EMBL; M13594; AAA60277.1; JOINED.
 DR EMBL; M13595; AAA60277.1; JOINED.
 DR EMBL; M13596; AAA60277.1; JOINED.

DR EMBL; M13597; AAA60277.1; JOINED.
 DR EMBL; M13598; AAA60277.1; JOINED.
 DR EMBL; M13880; AAA36580.1; ALT_TERM.
 DR PIR; A23223; TVHURK.
 DR PIR; A24421; TVHURK.
 DR HSSP; P08631; IAD5.
 DR MIM; 165020;
 DR InterPro; IPR000719; Euk PKinase.
 DR InterPro; IPR003964; FN_III.
 DR InterPro; IPR000033; Ldl_receptor_rep.
 DR InterPro; IPR002011; Receptor_tyr_kin_II.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00041; fn3; 7.
 DR Pfam; PF00069; pkinase; 1.
 DR SMART; SM00060; FN3; 5.
 DR SMART; SM00135; LY; 2.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
 KW Glycoprotein; ATP-binding; Phosphorylation; Proto-oncogene;
 KW Signal.
 FT CHAIN 1 27
 FT SIGNAL 1 27
 FT TRANSMEM 28 2347
 FT DOMAIN 1860 1859
 FT DOMAIN 1883 2347
 FT DOMAIN 1945 2222
 FT NP_BIND 1951 1959
 FT BINDING 1980 1980
 FT MOD_RES 2114 2114
 FT CARBOHYD 52 52
 FT CARBOHYD 114 114
 FT CARBOHYD 123 123
 FT CARBOHYD 324 324
 FT CARBOHYD 352 352
 FT CARBOHYD 366 366
 FT CARBOHYD 471 471
 FT CARBOHYD 607 607
 FT CARBOHYD 628 628
 FT CARBOHYD 706 706
 FT CARBOHYD 714 714
 FT CARBOHYD 732 732
 FT CARBOHYD 939 939
 FT CARBOHYD 961 961
 FT CARBOHYD 1015 1015
 FT CARBOHYD 1087 1087
 FT CARBOHYD 1090 1090
 FT CARBOHYD 1095 1095
 FT CARBOHYD 1211 1211
 FT CARBOHYD 1272 1272
 FT CARBOHYD 1330 1330
 FT CARBOHYD 1458 1458
 FT CARBOHYD 1461 1461
 FT CARBOHYD 1474 1474
 FT CARBOHYD 1499 1499
 FT CARBOHYD 1565 1565
 FT CARBOHYD 1669 1669
 FT CARBOHYD 1715 1715
 FT CARBOHYD 1738 1738
 FT CARBOHYD 1808 1808
 FT CONFLICT 2213 2213
 FT CONFLICT 2228 2229
 FT CONFLICT 2246 2259
 SQ SEQUENCE 2347 AA: 263956 MW: E14F3DFD10C1D2A CRC64;
 Query Match 63.6%; Score 35; DB 1; Length 2347;
 Best Local Similarity 55.6%; Pred. No. 81;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVFEAE 10
 Db 333 HQQVFESE 341

RESULT 21
 SLP_BACSU STANDARD; PRT; 124 AA.
 AC P39910;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 GN PAL-related lipoprotein precursor.
 SLP OR PAL.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Bacillus.
 NCBI_TaxID=1423;
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=90368558; PubMed=1697575;
 RA Hemilae H.O., Palva A., Paulin L., Ayyidson S., Palva I.;
 RT "Secretory S complex of Bacillus subtilis: sequence analysis and
 RT identity to pyruvate dehydrogenase.";
 RL J. Bacteriol. 172:5052-5063(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=92038903; PubMed=1936936;
 RA Hemilae H.;
 RT "Sequence of a PAL-related lipoprotein from Bacillus subtilis.";
 RL FEMS Microbiol. Lett. 66:37-41(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=97124187; PubMed=8969500;
 RA Witters P., Caldwell R.M., Enfield L., Ferrari E.;
 RT "The amp^s-nprE (124 degrees-127 degrees) region of the Bacillus
 RT subtilis 168 chromosome: sequencing of a 27 kb segment and
 RT identification of several genes in the area.";
 RL Microbiology 142:3033-3037(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=97124187; PubMed=8969500;
 RA Witters P., Caldwell R.M., Enfield L., Ferrari E.;
 RT "Sequence analysis of the mobA-amps region of the Bacillus subtilis
 RT chromosome.";
 RL submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 CC (Probable).
 CC -----
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 CC -----
 CC EMBL; M57435; AAA62685.1;
 DR EMBL; AF012285; AAC24936.1;
 DR EMBL; 299111; CAB13335.1;
 DR PIR; B54546; B54546.
 DR SUBSITE; BG10211; sfp.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Membrane; Lipoprotein; Signal; Complete proteome.
 FT SIGNAL 1 18
 FT CHAIN 19 124 POTENTIAL.
 FT LIPID 19 19 PAL-RELATED LIPOPROTEIN.
 FT SEQUENCE 124 AA; 14538 MW; 804401AFOE88446F CRC64;

Query Match 61.88; Score 34; DB 1; Length 124;
 Best Local Similarity 40.08; Pred. No. 6.3;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 OY 1 HHOKLVFEAE 10
 Db 36 HHTQVFESE 45

RESULT 22
 YNS1_YEAST STANDARD; PRT; 763 AA.
 ID YNS1_YEAST
 AC P42843;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 GN Hypothetical 88.9 kDa protein in RPR2-STBI intergenic region.
 GN YNL311C OR N0376.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / FY1676;
 RX MEDLINE=96076632; PubMed=7502583;
 RA Maftahl M., Nicoud J.-M., Levesque H., Galliard C.;
 RT "Sequencing analysis of a 24.7 kb fragment of yeast chromosome XIV
 RT identifies six known genes, a new member of the hexose transporter
 RT family and ten new open reading frames.";
 RL Yeast 11:1077-1085(1995).
 RN [2]
 RP SEQUENCE OF 149-763 FROM N.A.
 RA Maurer C.T.C., Urbanus J.H.M., Planta R.J.;
 RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; Z46259; CAA6384.1;
 DR EMBL; Z71587; CAA96240.1;
 DR SGD; S0005255; YNL311C.
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.
 DR SMART; SM00256; FBOX; 1.
 DR PROSITE; PS50181; FBOX; 1.
 KW Hypothetical protein.
 FT DOMAIN 54 100 F-BOX.
 FT DOMAIN 22 28 POLY-GLU.
 FT SEQUENCE 763 AA; 88941 MW; 81102168449051BC CRC64;
 SQ
 Query Match 61.88; Score 34; DB 1; Length 763;
 Best Local Similarity 100.08; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHOKLV 6
 Db 323 HHOKLV 328

RESULT 23
 RPOD_PEA STANDARD; PRT; 1163 AA.
 ID RPOD_PEA
 AC P12227;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-1993 (Rel. 26, Last annotation update)

DE DNA-directed RNA polymerase beta" chain (EC 2.7.7.6) (Fragment).
GN RPOC2.
OS Pisum sativum (Garden pea).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC easterids I; Fabales; Falcaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86323089; PubMed=3530249;
RA Correns A.L., Walker J.E.;
RT "Pea chloroplast DNA encodes homologues of Escherichia coli ribosomal
subunit S2 and the beta-subunit of RNA polymerase.";
RL Biochem. J. 236:453-460(1986).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
(RNA)(N).
CC -1- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
SUBUNITS: ALPHA, BETA, BETA', AND BETA".
CC -----
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CC -----
DR EMBL: X03912; CAA27545.1; -
DR PIR: S07137; S07137.
DR Mendel: 5368; PISsat;RPOC2.1.
KW Transferase; Transcription; DNA-directed RNA polymerase; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 1163 AA; 133598 MW; C92E7BE0A3DB55 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 1163;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 HHOKLVFA 9
DB 1149 HHKILDFFA 1157

RESULT 24
ROM2_YEAST STANDARD; PRT; 1356 AA.
ID ROM2_YEAST
AC P51862;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE RHO1 GDP-GTP exchange Protein 2.
GN ROM2 OR YLR371W OR L8039.3.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Pavello A., Fulton L., Gattung S., Greco T., Kirsten J.,
RA Kueba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA Maritz E., Meneses S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Rifken L., Riles L., Trevaas E., Vignati D.,
RA Wilcox L., Woldman P., Vaudin M., Wilson R., Waterston R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RA [2]
RA CHARACTERIZATION.

RX MEDLINE=96208506; PubMed=8641285;
RA Ozaki K., Tanaka K., Imamura H., Hihara T., Kameyama T.,
RA Nonaka H., Hirano H., Matsura Y., Takai Y.;
RT "Rom1p and Rom2p are GDP/GTP exchange proteins (GEPs) for the Rho1p
small GTP binding protein in Saccharomyces cerevisiae.";
RL EMBO J. 15:2196-2207(1996).
CC -1- FUNCTION: STIMULATES THE EXCHANGE OF RHO1 GDP-BOUND FORM INTO
GTP-BOUND FORM.
CC -1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
CC -----
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CC -----
DR EMBL: U19103; AAB67564.1; -
DR SGD: S0004363; ROM2.
DR InterPro: IPR001180; CNH.
DR InterPro: IPR000591; DEP.
DR InterPro: IPR000219; RhoGEF.
DR Pfam: PF00780; CNH; 1.
DR Pfam: PF00610; DEP; 1.
DR Pfam: PF00621; RhoGEF; 1.
DR SMART: SM00036; CNH; 1.
DR SMART: SM00049; DEP; 1.
DR SMART: SM00325; RhoGEF; 1.
DR PROSITE: PS00741; DH_1; FALSE_NEG.
DR PROSITE: PS50010; DH_2; 1.
KW Guanine-nucleotide releasing factor.
FT DOMAIN 659 846
FT DOMAIN 252 265
FT DOMAIN 329 336
FT DOMAIN 632 635
SQ SEQUENCE 1356 AA; 152595 MW; 5FBC542114E7BC92 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 1356;
Best Local Similarity 50.0%; Pred. No. 73;
Matches 7; Conservative 3; Mismatches 0; Indels 4; Gaps 1;
QY 1 HHOKLV---FFAE 10
DB 1131 HHKELINHSFFAE 1144

RESULT 25
TRX2_HUMAN STANDARD; PRT; 2715 AA.
ID TRX2_HUMAN
AC Q9UNM6; Q9UNK25; Q95836; Q9Y669; Q9Y668; O15022;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Trithorax homolog 2 (Mixed lineage leukemia gene homolog 2 protein).
GN TRX2 OR HRX2 OR MLL2 OR KIA0340.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RA Angrand P.O., Valvatne H., Jeanmougin F., Adamson A.,
RA van der Hoeven F., Olsen L., Tekotte H., Huang N., Poch O.,
RA Lamerdin J., Chabon P., Losson R., Stewart A., Asaland R.;
RT "Mammalian trithorax- and ASH1-like proteins: putative chromatin
regulators which contain PHD fingers and SET domains.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RA Lamerdin J.E., McCreedy P.M., Adamson A.W., Burkhart-Schultz K.,
RA Garcia E., Kyle A., Ramirez M., Stillwagen S., Ganes J., Danganan L.,
RA Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,

RA Carrano A.V.:
 RT "Sequence analysis of a 1 Mb region in human 19q13.1."
 RL Submitted (NOV 1996) to the EMBL/Genbank/DBJ databases.
 RN [1]
 RP SEQUENCE OF 816-2715 FROM N.A. (LONG ISOFORM).
 RC TISSUE=Brain;
 RA MEDLINE=9734984; PubMed=9205841;
 RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. VII.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro."
 RL DNA Res. 4:141-150(1997).
 RN [4]
 RP SEQUENCE OF 111-2715 FROM N.A. (LONG ISOFORM).
 RC TISSUE=Testis, and Leukocyte;
 RA MEDLINE=20105772; PubMed=10637508;
 RA Huntsman D.G., Chin S.-F., Mulieris M., Batley S.J., Collins V.P.,
 RA Wiedemann L.M., Aparicio S., Caldas C.;
 RT "ML2, the second human homolog of the Drosophila trithorax gene, maps
 RT to 19q13.1 and is amplified in solid tumor cell lines."
 RL Oncogene 18:7975-7984(1999).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A. (LONG AND TRUNCATED ISOFORMS).
 RC TISSUE=Placenta, and Bone marrow;
 RA MEDLINE=9933983; PubMed=10409430;
 RA Fitzgerald K.T., Diaz M.O.;
 RT "ML2: A new mammalian member of the trx/MLL family of genes."
 RL Genomics 59:187-192(1999).
 CC -1- FUNCTION: POSSIBLY ACTS AS A TRANSCRIPTIONAL REGULATORY FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 CC TRUNCATED FORM. ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVELS IN TESTIS.
 CC ALSO FOUND IN BRAIN, BONE MARROW, HEART, MUSCLE, KIDNEY, PANCREAS,
 CC SPLEEN, THYMUS, PROSTATE, OVARY, INTESTINE, COLON, PERIPHERAL
 CC BLOOD LYMPHOCYTES, AND PLACENTA.
 CC -1- DISEASE: OFTEN AMPLIFIED IN PANCREATIC CARCINOMAS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSCRIPTION FACTOR TRITHORAX FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BROMODOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SET DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 PHD-TYPE ZINC FINGERS.
 CC -1- SIMILARITY: CONTAINS 1 CXXC-TYPE ZINC FINGER.
 CC -----
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 CC -----
 DR EMBL: AJ007041; CAB45385.1;
 DR EMBL: AB000671; -; NOT_ANNOTATED_CDS.
 DR EMBL: AB002302; BAA20763.2;
 DR EMBL: AF186605; AAD56420.1;
 DR EMBL: AF104918; AAD17932.1;
 DR EMBL: AF105279; AAD26113.1;
 DR EMBL: AF105280; AAD26112.1;
 DR InterPro: IPR000637; AT_hook.
 DR InterPro: IPR003889; FYrich.C.
 DR InterPro: IPR003888; FYrich.N.
 DR InterPro: IPR001965; PHD.
 DR InterPro: IPR003616; PostSET.
 DR InterPro: IPR001214; SET.
 DR InterPro: IPR002857; znf-CXXC.
 DR InterPro: IPR001841; znf_ring.
 DR Pfam: PF00628; PHD; 3.
 DR Pfam: PF00856; SET; 1.
 DR Pfam: PF02008; zf-CXXC; 1.
 DR SMART: SM00384; AT_hook; 1.
 DR SMART: SM00542; FYRC; 1.
 DR SMART: SM00541; FYRN; 1.

DR SMART: SM00249; PHD; 4.
 DR SMART: SM00508; PostSET; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00317; SET; 1.
 DR PROSITE: PS0280; SET; 1.
 KM DNA-binding; Bromodomain; Nuclear protein; Zinc-finger; Metal-binding;
 KM Transcription regulation; Alternative splicing.
 FT DNA_BIND 37 44
 FT DNA_BIND 110 117
 FT DNA_BIND 357 365
 FT ZN_FING 959 1005
 FT ZN_FING 1203 1252
 FT ZN_FING 1253 1303
 FT ZN_FING 1337 1396
 FT ZN_FING 1449 1471
 FT DOMAIN 2586 2715
 FT DOMAIN 26 37
 FT DOMAIN 248 255
 FT DOMAIN 362 398
 FT DOMAIN 402 771
 FT DOMAIN 808 812
 FT DOMAIN 1963 1970
 FT DOMAIN 2251 2259
 FT VARSPLIC 532 582
 FT FT
 FT FT
 FT VARSPLIC 583 2715
 FT CONFLICT 834 834
 FT CONFLICT 941 941
 FT CONFLICT 1317 1317
 FT CONFLICT 1362 1362
 FT CONFLICT 1438 1438
 FT CONFLICT 2622 2622
 SO SEQUENCE 2715 AA; 293511 MW; C0615B981BBE7BF CRC64;
 Query Match Best Local Similarity 61.88; Score 34; DB 1; Length 2715;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 HNKIVFEAE 10
 Db 2468 HDAVITLAE 2477
 RESULT 26
 PKSL_BACSU STANDARD; PRT; 4427 AA.
 AC 005470;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Putative polyketide synthase pksl (PKS).
 GN PKSL OR PKSX OR PKSA OR OUTG.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/staphylococcus group; Bacillus.
 CX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / PB1424;
 RX MEDLINE=93345824; PubMed=8344529;
 RA Scott C., Platt M., Guzman A., Perani P., Tognoni A., Grandi G.,
 RA Galizzi A., Albertini A.M.;
 RT "A Bacillus subtilis large ORF coding for a polypeptide highly
 RT similar to polyketide synthases."
 RL gene 130:65-71(1993).
 RN [2]
 RP SEQUENCE OF 3619-4427 FROM N.A.
 RC STRAIN=168 / PB1424;
 RA Grandi G.;
 RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: POTENTIALLY INVOLVED IN SOME INTERMEDIATE STEPS FOR

CC THE SYNTHESIS OF A POLYKETIDE MOLECULE WHICH MAY BE INVOLVED IN
 CC SECONDARY METABOLISM.
 CC -1- COFACTOR: CONTAINS 5 COVALENTLY BOUND PHOSPHOPANTETHEINES
 CC (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS 5 ACYL CARRIER DOMAINS.
 CC
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 CC
 CC -----
 CC EMBL: Z14098; CA878479.1; -
 CC EMBL: U11039; AA85145.1; -
 CC EMBL: Z35133; CA88504.1; -
 CC EMBL: Z99113; CAB13602.1; -
 CC PIR: S25021; S25021.
 CC HSP: P27796; IPI.
 CC Subtilist: BG10698; PKSL.
 CC InterPro: IPR000794; Ketocacyl-synt.
 CC InterPro: IPR003880; PhosphopantL-attach.
 CC Pfam: PF00109; Ketocacyl-synt_4.
 CC Pfam: PF00550; pp-binding_5.
 CC PROSITE: PS00012; PHOSPHOPANTETHEINE; 5.
 CC PROSITE: PS00606; B-KETOCACYL-SYNTHASE; 1.
 CC PROSITE: PS50075; ACP-DOMAIN; 5.
 CC K: Transferrase; Acyltransferase; Antibiotic biosynthesis; NADP;
 CC KM Phosphopantetheine; Multifunctional enzyme; Repeat; Complete proteome.
 CC FT DOMAIN 211 280 ACYL CARRIER (ACP) 1.
 CC FT DOMAIN 382 759 BETA-KETOCACYL SYNTHASE 1.
 CC FT DOMAIN 937 1115 DEHYDRATASE.
 CC FT DOMAIN 1409 1602 BETA-KETOCACYL REDUCTASE 1.
 CC FT DOMAIN 1687 1759 ACYL CARRIER (ACP) 2.
 CC FT DOMAIN 1876 2253 BETA-KETOCACYL SYNTHASE 2.
 CC FT DOMAIN 2491 2560 ACYL CARRIER (ACP) 3.
 CC FT DOMAIN 2632 2701 ACYL CARRIER (ACP) 4.
 CC FT DOMAIN 2823 3182 BETA-KETOCACYL SYNTHASE 3.
 CC FT DOMAIN 3575 3776 BETA-KETOCACYL REDUCTASE 2.
 CC FT DOMAIN 3854 3923 ACYL CARRIER (ACP) 5.
 CC FT DOMAIN 4019 4373 BETA-KETOCACYL SYNTHASE 4.
 CC FT BINDING 243 243 PHOSPHOPANTETHEINE (POTENTIAL).
 CC FT BINDING 1723 1723 PHOSPHOPANTETHEINE (POTENTIAL).
 CC FT BINDING 2523 2523 PHOSPHOPANTETHEINE (POTENTIAL).
 CC FT BINDING 2664 2664 PHOSPHOPANTETHEINE (POTENTIAL).
 CC FT BINDING 3886 3886 PHOSPHOPANTETHEINE (POTENTIAL).
 CC SQ SEQUENCE 4427 AA; 493398 MW; 9612521E561AB9F2 CRC64;
 CC
 CC Query Match 61.8%; Score 34; DB 1; Length 4427;
 CC Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 HHOKLV 6
 CC Db 691 HHOKLV 696
 CC
 CC RESULT 27
 CC ACUB_BACSU STANDARD; PRT; 214 AA.
 CC AC P39066;
 CC DT 01-FEB-1995 (Rel. 31, Created)
 CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Acetoin utilization acub protein.
 CC GN ACUB.
 CC OS Bacillus subtilis.
 CC OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC OC Bacillus/Staphylococcus group; Bacillus.
 CC OX NCBI_TaxID=1423;
 CC [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=95020526; Pubmed=7934817;
 RA Grundy F.J., Waters D.A., Takova T.Y., Henkin T.M.;
 RT "Identification of genes involved in utilization of acetate and
 RT acetoin in Bacillus subtilis."
 RT Mol. Microbiol. 10:259-271(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98048467; Pubmed=9387221;
 RA Lepidus A., Galleron N., Sorokin A., Ehrlich S.D.;
 RT "Sequencing and functional annotation of the Bacillus subtilis genes
 RT in the 200 kb rnb-dnaB region."
 RT Microbiology 143:3431-3441(1997).
 CC -1- FUNCTION: ROLE IN GROWTH AND SPOURATION ON ACETOIN OR BUTANEDIOL.
 CC INVOLVED IN THE BREAKDOWN OF THESE COMPOUNDS USED AS A CARBON
 CC SOURCE.
 CC
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC
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 CC
 CC -----
 CC EMBL: L17309; AA68285.1; -
 CC EMBL: AF008220; AAC00395.1; -
 CC EMBL: Z99119; CAB1948.1; -
 CC PIR: S39644; S39644.
 CC Subtilist: BG10368; acb.
 CC InterPro: IPR002912; ACT.
 CC InterPro: IPR00644; CBS.
 CC Pfam: PF01842; ACT; 1.
 CC Pfam: PF00571; CBS; 2.
 CC SMART: SM00116; CBS; 2.
 CC Sporulation; Repeat; CBS domain; Complete proteome.
 CC FT DOMAIN 5 58 CBS 1.
 CC FT DOMAIN 75 128 CBS 2.
 CC SQ SEQUENCE 214 AA; 24351 MW; 3B7A964B5C95CECF CRC64;
 CC
 CC Query Match 60.0%; Score 33; DB 1; Length 214;
 CC Best Local Similarity 83.3%; Pred. No. 17;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 HHOKLV 6
 CC Db 110 HHOKLV 115
 CC
 CC RESULT 28
 CC PPNK_THEMA STANDARD; PRT; 258 AA.
 CC ID PPNK_THEMA
 CC AC Q9X255;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Probable inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23)
 CC DE (Poly(P)/ATP NAD kinase).
 CC GN PPNK OR TM173.
 CC OS Thermotoga maritima.
 CC OC Bacteria; Thermotogales; Thermotoga.
 CC OX NCBI_TaxID=2336;
 CC [1]
 CC SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=99287316; Pubmed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Uitterlind T.R., Malek J.A., Liner K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RL genome sequence of *Thermotoga maritima*.";
 CC Nature 396:323-329(1999).
 CC -1- FUNCTION: Catalyzes the phosphorylation of NAD to NADP. Utilizes
 CC ATP and other nucleoside triphosphates as well as inorganic
 CC polyphosphate as a source of phosphorus (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + NAD(+) -> ADP + NADP(+).
 CC -1- COFACTOR: Requires divalent metal ions for activity (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE NAD KINASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE001812; AAD36798.1; -
 CC TIGR: TM1733; -
 CC InterPro: IPR002504; DUF15.
 CC Pfam: PF01513; DUF15; 1.
 CC Kinase: Kinase; NADP; Complete proteome.
 CC TRANSFERASE; Kinase; NADP; Complete proteome.
 CC SEQUENCE 258 AA; 29241 MW; 45EBBCA086FDEAB CRC64;

Query Match 60.0%; Score 33; DB 1; Length 258;
 Best Local Similarity 50.0%; Pred. No. 21;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HHQKLVFAE 10
 Db 140 HHSMWFFAD 149

RESULT 29
 ID 1105_HUMAN STANDARD: PRT; 325 AA.
 AC Q08334;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Interleukin-10 receptor beta chain precursor (IL-10R-B) (IL-10R2)
 DE (Cytokine receptor class-II CRF2-4).
 GN IL10RB OR CRF24.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=93300510; PubMed=8314576;
 RA Lutfalla G., Gardiner K., Uze G.;
 RT "A new member of the cytokine receptor gene family maps on chromosome
 RT 21 at less than 35 kb from IFNAR.";
 RL Genomics 16:366-373(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96054036; PubMed=7563119;
 RA Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
 RT "Structure of the human CRFB4 gene: comparison with its IFNAR
 RT neighbor.";
 RL J. Mol. Evol. 41:338-344(1995).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=87459974; PubMed=9312047;
 RA Kotelko S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu W.,
 RA Pestka S.;
 RT "Identification and functional characterization of a second chain of
 RT the Interleukin-10 receptor complex.";

RL EMBL J. 16:5894-5903(1997).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=20469498; PubMed=10875937;
 RA Xie M.-H., Aggarwal S., Ho W.-H., Foster J., Zhang Z., Stinson J.,
 RA Wood W.T., Godard A.D., Guiney A.L.;
 RT "Interleukin (IL)-22, a novel human cytokine that signals through the
 RT interferon receptor-related proteins CRF2-4 and IL-22R.";
 RL J. Biol. Chem. 275:31335-31339(2000).
 CC -1- FUNCTION: RECEPTOR FOR IL-10 AND IL-22. SERVES AS AN ACCESSORY
 CC CHAIN ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO
 CC INITIATE IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: Z17237; CA78933.1; -
 CC EMBL: U08968; AAA86872.1; -
 CC PIR: A47003; A47003.
 CC HSSP: P13726; ITFH.
 CC MIM: 123889; -
 CC InterPro: IPR000282; Cytok_receptor_2.
 CC DR InterPro: IPR001187; Tissue_fac.
 CC DR Pfam: PF01108; Tissue_fac; 1.
 CC KW Receptor; Transmembrane; Glycoprotein; Signal.
 CC FT SIGNAL 1 19
 CC FT CHAIN 20 325
 CC FT DOMAIN 20 220
 CC FT TRANSMEM 221 242
 CC FT DOMAIN 243 325
 CC FT DOMAIN 113 205
 CC FT DISULFID 66 74
 CC FT DISULFID 188 209
 CC FT CARBOHYD 49 49
 CC FT CARBOHYD 68 68
 CC FT CARBOHYD 102 102
 CC FT CARBOHYD 161 161
 CC FT CONFLICT 124 124
 CC FT CONFLICT 269 273
 CC FT CONFLICT 274 325
 CC FT SEQUENCE 325 AA; 37011 MW; 66706C79F8514B23 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 325;
 Best Local Similarity 55.6%; Pred. No. 27;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HHQKLVFAE 9
 Db 274 HHNTLFFS 282

RESULT 30
 ID C7D9_SOYBN STANDARD: PRT; 496 AA.
 AC 081971;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cytochrome P450 71D9 (EC 1.14.-.-) (P450 CP3).
 GN CYP71D9.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OC NCBI_TaxID=3847;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, HAROSY 63;
RX MEDLINE-98311068; PubMed-9648734;
RA Schopfer C.R., Edel J.;
RT "Identification of elicitor-induced cytochrome P450s of soybean
  (glycine max L.) using differential display of mRNA.";
RL Mol. Gen. Genet. 258:315-322(1998).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC or send an email to license@isb-slb.ch).
CC -----
CC EMBL: Y10490; CAA71514.1;
CC InterPro: IPR001128; CYT_P450.
CC Pfam: PF00067; P450.1.
CC PROSITE: PS00086; CYTOCHROME_P450.1.
CC Oxidoreductase; Monooxygenase; Heme.
CC BINDING 437 437 HEME (BY SIMILARITY).
CC SEQUENCE 496 AA; 56205 MW; 9C90947C8A546CE1 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 496;
Best Local Similarity 83.3%; Pred. NO. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLV 6
DB 197 HHOKLI 202

RESULT 31
G6PI_HAETIN STANDARD; PRT; 549 AA.
ID G6PI_HAETIN STANDARD; PRT; 549 AA.
AC P44312;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN PGI OR H11576.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RD / KW20 / ATCC 51907;
RX MEDLINE-95350630; PubMed-7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Iu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
RA Fline L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:96-112(1995).
CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate -> D-fructose 6-
CC phosphate.
CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONOGENESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (By similarity).
CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC -----
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CC -----
CC EMBL: U32831; AAC23219.1; ALT_INIT.
CC TIGR: H11576.
CC InterPro: IPR001672; G6P_Isomerase.
CC Pfam: PF00342; PGI.1.
CC PRINTS: PR00662; G6PIISOMERASE.
CC PROSITE: PS00765; P_GLUCOSE_ISOMERASE_1; 1.
CC PROSITE: PS00174; P_GLUCOSE_ISOMERASE_2; 1.
CC Isomerase; Glucosogenesis; Glycolysis; Complete proteome.
CC ACT_SITE 387 387 BY SIMILARITY.
CC ACT_SITE 515 515 BY SIMILARITY.
CC SEQUENCE 549 AA; 61622 MW; F6534C667068F16 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 549;
Best Local Similarity 58.3%; Pred. NO. 46;
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
DB 417 HHNKLI--FFAQ 428

RESULT 32
STT_MYGE STANDARD; PRT; 564 AA.
ID STT_MYGE STANDARD; PRT; 564 AA.
AC P47615;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase)
DE (Thrs).
GN THRS OR MG375.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 33530 / G-37;
RX MEDLINE-96026346; PubMed-7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Uterback T.R., Sauder D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 350-463 FROM N.A.
RC STRAIN-ATCC 33530 / G-37;
RX MEDLINE-94075230; PubMed-8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
RT sequencing.";
RL J. Bacteriol. 175:7918-7930(1993).
CC -1- CATALYTIC ACTIVITY: ATP + L-threonine + tRNA(Thr) -> AMP +
CC diphosphate + L-threonyl-tRNA(Thr).
CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-tRNA SYNTHETASE FAMILY.
CC -----
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CC -----

DR EMBL: U93719; AAC71602.1; -

DR EMBL: U02130; AAD12408.1; -

DR HSSP: P00955; LEVL.

DR TIGR: MG375; -

DR InterPro: IPR002106; AA-trna_ligase_II.

DR InterPro: IPR004154; HGT-anticodon.

DR InterPro: IPR002314; tRNA-synt_2p.

DR InterPro: IPR003320; tRNA-synt_1tr.

DR Pfam: PF03129; HGT-anticodon; 1.

DR Pfam: PF00587; tRNA-synt_2p; 1.

DR PRINTS: PRO1047; TRNASYNTHTR.

DR PROSITE: PS00179; AA-trna_ligase_II.1; FALSE_NEG.

DR PROSITE: PS00339; AA-trna_ligase_II.2; FALSE_NEG.

KM Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Metal-binding; Zinc; Complete proteome.

FT DOMAIN 167 464 CATALYTIC.

FT METAL 260 260 ZINC (CATALYTIC) (BY SIMILARITY).

FT METAL 311 311 ZINC (CATALYTIC) (BY SIMILARITY).

FT METAL 441 441 ZINC (CATALYTIC) (BY SIMILARITY).

SO SEQUENCE 564 AA; 65595 MW; 2CA833DA/F7AC447 CRC64;

Query Match

Best Local Similarity 71.4%; Score 33; DB 1; Length 564;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVF 7

DB 207 HHQOLLF 213

RESULT 33

SDC3_CAEEL STANDARD; PRT; 2150 AA.

ID SDC3_CAEEL

AC P34706;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Zinc finger protein sdc-3.

GN SDC-3.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Pelodermidae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RX MEDLINE-93161411; PubMed-8431944;

RA Klein R.D., Meyer B.J.,

RT "Independent domains of the Sdc-3 protein control sex determination and dosage compensation in C. elegans."

RL Cell 72:349-364(1993).

-1- FUNCTION: CONTROLS BOTH SEX DETERMINATION AND X CHROMOSOME DOSAGE COMPENSATION. THESE TWO FUNCTIONS ACT INDEPENDENTLY.

-1- SUBCELLULAR LOCATION: Nuclear.

-1- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYONIC AND EARLY LARVAL STAGES.

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CC -----

DR EMBL: M85149; AAA28144.1; -

DR PIR: S27802; S27802.

DR InterPro: IPR000822; Znf-C2H2.

DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 1.

DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; FALSE_NEG.

KM Developmental protein; Zinc-finger; Metal-binding; DNA-binding;

KW Nuclear protein; Repeat.

FT DOMAIN 443 987

FT DOMAIN 1508 1516 DOSAGE COMPENSATION DOMAIN 1.

FT DOMAIN 2080 2105 SEX DETERMINATION DOMAIN.

FT ZN_FING 2078 2105 DOSAGE COMPENSATION DOMAIN 2.

FT ZN_FING 2117 2141 C2H2-TYPE.

FT ZN_FING 2117 2141 C2H2-TYPE.

SO SEQUENCE 2150 AA; 249954 MW; 7430D77AC784EA46 CRC64;

Query Match

Best Local Similarity 60.0%; Score 33; DB 1; Length 2150;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10

DB 2140 HHSRRCFFAD 2149

RESULT 34

G6PI_KLEOX STANDARD; PRT; 167 AA.

ID G6PI_KLEOX

AC P77877;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (Pgi) (Phosphohexose isomerase) (PHI) (Fragment).

GN PGI.

OS Klebsiella oxytoca.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Klebsiella.

OX NCBI_TaxID=571;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-EA321;

RX MEDLINE-97032593; PubMed-8875859;

RA Katz L.A.,

RT "Transkingdom transfer of the phosphoglucose isomerase gene."

RL J. Mol. Evol. 43:453-459(1996).

-1- CATALYTIC ACTIVITY: D-glucose 6-phosphate -> D-fructose 6-phosphate.

-1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.

-1- SUBCELLULAR LOCATION: Cytoplasmic.

-1- SIMILARITY: BELONGS TO THE GPI FAMILY.

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CC -----

DR EMBL: U54763; AAB50058.1; -

DR InterPro: IPR001672; G6P_Isomerase.

DR Pfam: PF00342; PGI; 1.

DR PROSITE: PS00765; P-GLUCOSE ISOMERASE_1; PARTIAL.

DR PROSITE: PS00174; P-GLUCOSE ISOMERASE_2; PARTIAL.

KW Isomerase; Gluconeogenesis; Glycolysis.

FT NON_TER 1 1

FT NON_TER 167 167

SO SEQUENCE 167 AA; 18875 MW; F6C56A969F06F891 CRC64;

Query Match

Best Local Similarity 58.2%; Score 32; DB 1; Length 167;

Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 HHOKLV-FFAE 10

DB 115 HHPKLSNFFAQ 126

RESULT 35

CALC_MOUSE
ID CALC_MOUSE STANDARD; PRT; 178 AA.
AC 063811;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcineurin B subunit isoform 2 (Protein phosphatase 2B regulatory subunit 2) (Protein phosphatase 3 regulatory subunit B alpha isoform 2).
GN PPP3R2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
(1)
RP SEQUENCE FROM N.A.
RX MEDLINE-92392379; PubMed-1325794;
RT Ueki K., Muramatsu T., Kincaid R.L.;
RT "Structure and expression of two isoforms of the murine calmodulin-dependent protein phosphatase regulatory subunit (calcineurin B).";
RT Biochem. Biophys. Res. Commun. 187:537-543(1992).
CC -1- FUNCTION: REGULATORY SUBUNIT OF CALCINEURIN, A CALCIUM-DEPENDENT, CALMODULIN STIMULATED PROTEIN PHOSPHATASE. CONFERS CALCIUM SENSITIVITY.
CC -1- SUBUNIT: COMPOSED OF A CATALYTIC SUBUNIT (A) AND A REGULATORY SUBUNIT (B).
CC -1- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
CC -1- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING SITES.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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CC EMBL; S43865; AAB23172.1; -
CC DR HSSP; P06705; ITCO.
DR GSD; MGI:107171; Pp3r2.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR001125; Recoverin.
DR Pfam; PF00036; efhand; 4.
DR PRINTS; PR00450; RECOVERIN.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF_HAND; 4.
KW Calcium-binding; Repeat; Myristate.
KW INT_MET 0 BY SIMILARITY.
FT LIPID 1 MYRISTATE (BY SIMILARITY).
FT CA_BIND 30 41 EF-HAND 1.
FT CA_BIND 62 73 EF-HAND 2.
FT CA_BIND 99 110 EF-HAND 3.
FT CA_BIND 140 151 EF-HAND 4.
SQ SEQUENCE 178 AA; 20528 MW; F453B9A047C240F5 CRC64;

Query Match 58.2%; Score 32; DB 1; Length 178;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 HOKLVEFAE 10
Db 162 HKKLVYFE 170

RESULT 36
ID CYF_GUTTH STANDARD; PRT; 321 AA.
AC 078494;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Apocytochrome F precursor.
GN PETA.
OS Guillardia theta (Cryptomonas phi).
OG Chloroplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
(1)
RP SEQUENCE FROM N.A.
RX MEDLINE-99128221; PubMed-9929392;
RA Douglas S.E., Penny S.L.;
RT "The complete genome of the cryptophyte alga, Guillardia theta: complete sequence and conserved synteny groups confirm its common ancestry with red algae.";
RT J. Mol. Evol. 48:236-244(1999).
CC -1- FUNCTION: TRANSLOCATES PROTONS ACROSS THE THYLAKOID MEMBRANE AND RECEIVES ELECTRONS FROM PHOTOSYSTEM II TO PHOTOSYSTEM I. IT THEM TO PLASTOCYANIN. THIS FUNCTION IS VERY SIMILAR TO THAT OF MITOCHONDRIAL CYTOCHROME C1.
CC -1- SUBUNIT: MEMBER OF THE CYTOCHROME B6/F COMPLEX INCLUDING CYTOCHROME B6, CYTOCHROME F AND PROBABLY AN IRON SULFUR PROTEIN.
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane (Probable).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C FAMILY.
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CC EMBL; AF041468; AAC35685.1; -
CC DR HSSP; P36438; IHCZ.
DR InterPro; IPR002325; Apocyt_F.
DR InterPro; IPR000345; CytC_heme_bind.
DR Pfam; PF01333; Apocytochrome_F; 1.
DR PRINTS; PR00610; CYTOCHROME_F.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
KW Electron transport; Heme; Chloroplast; Thylakoid; Photosynthesis; Photosystem I; Photosystem II; Transit peptide.
KW Transmembrane.
KW TRANSIT 1
FT CHAIN 39 321 CHLOROPLAST (BY SIMILARITY).
FT BINDING 59 59 APOCYTOCHROME F.
FT BINDING 62 62 HEME (COVALENT) (PROBABLE).
FT METAL 63 63 HEME (COVALENT) (PROBABLE).
FT TRANSMEM 287 307 IRON (HEME AXIAL LIGAND) (PROBABLE).
SQ SEQUENCE 321 AA; 35173 MW; 42A1FF89FB05AE3D CRC64;

Query Match 58.2%; Score 32; DB 1; Length 321;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVE 7
Db 161 HOKLVE 166

RESULT 37
ID FD3E_SOYBN STANDARD; PRT; 380 AA.
AC P48625;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.99.-).
GN FAD3.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;

[1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-Seed;
 RX MEDLINE-94302147; PubMed-8029334;
 RA Yedav N.S., Wierzbicki A., Aegeerter M., Caster C.S., Perez-Grau L.,
 RA Kliney A.J., Hitz W.D., Booth J.R. Jr., Schweigler B., Stecca K.L.,
 RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
 RA Feldmann K.A., Pierce J., Browne J.;
 RT "Cloning of higher plant omega-3 fatty acid desaturases";
 RL Plant Physiol. 103:467-476(1993).
 CC -1- FUNCTION: MICROSOXIAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTRAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: L22964; AAA61777.1; -
 DR PIR: JQ2338; JQ2338.
 DR InterPro: IPR001225; FA_desaturase.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR ProDom: PD001081; FA_desaturase; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 KW Transmembrane
 FT TRANSMEM 55 75 POTENTIAL.
 FT TRANSMEM 212 232 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 FT DOMAIN 100 104 HISTIDINE BOX 1.
 FT DOMAIN 136 140 HISTIDINE BOX 2.
 FT DOMAIN 303 307 HISTIDINE BOX 3.
 SQ SEQUENCE 380 AA; 44185 MW; BF800F93CFC2907 CRC64;
 Query Match 58.2%; Score 32; DB 1; Length 380;
 Best Local Similarity 62.5%; Pred. No. 50;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 1 HHOKLVEF 8
 DB 264 HHOKLPMY 271
 RESULT 38
 LBP_HUMAN STANDARD; PRT; 481 AA.
 AC PI8428; Q92672; Q43438; Q9UD66; Q9H403;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Lipopolysaccharide-binding protein precursor (LBP).
 GN LBP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-90385281; PubMed-2402637;
 RA Schumann R.R., Leong S.R., Flagg G.W., Gray P.W., Wright S.D.,
 RA Mathison J.C., Tobias P.S., Ulevitch R.J.;
 RT "Structure and function of lipopolysaccharide binding protein.";

RL Science 249:1429-1431(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94292492; PubMed-7517398;
 RA Wilde C.G., Sellhammer J.J., McGrohan M., Ashton N., Snable J.L.,
 RA Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;
 RT "Bactericidal/permeability-increasing protein and lipopolysaccharide
 RT (LPS)-binding protein. LPS binding properties and effects on LPS-
 RT mediated cell activation";
 RL J. Biol. Chem. 269:17411-17416(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Hudacek J.A., Aslanidis C., Schmitz G.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96110577; PubMed-9441745;
 RA Kirschning C.J., Au-Young J., Lamping N., Reuter D., Pfeil D.,
 RA Sellhammer J.J., Schumann R.R.;
 RT "Similar organization of the lipopolysaccharide-binding protein (LBP)
 RT and phospholipid transfer protein (PLTP) genes suggests a common gene
 RT family of lipid-binding proteins";
 RL Genomics 46:416-425(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RA Long J.Y., Liu J.Q., Xue Y.N., Wang H.X.;
 RT "Cloning and sequencing of human lipopolysaccharide-binding protein
 RT gene";
 RL Shang Wu Huaxue Yu Shengwu Wuli Jinzhan 25:469-471(1998).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A.C., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Laylor S.,
 RA Levasallo M.H., Levesha M., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McKay D., McMurtry A.A.,
 RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Sruce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann M., Sycomore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitteker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20";
 RL Nature 414:865-871(2001).
 RN [7]
 RP SEQUENCE OF 1-41 FROM N.A.
 RA Sutton C.L., Smith R.I.F., Centola M.B., Theofan G.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE-98227852; PubMed-9568897;
 RA Beamer L.J., Carroll S.F., Eisenberg D.;
 RT "The BPI/LBP family of proteins: a structural analysis of conserved
 RT regions";
 RL Protein Sci. 7:906-914(1998).
 CC -1- FUNCTION: BINDS TO THE LIPID A MOIETY OF BACTERIAL
 CC LIPOPOLYSACCHARIDES (LPS), A GLYCOLIPID PRESENT IN THE OUTER
 CC MEMBRANE OF ALL GRAM-NEGATIVE BACTERIA. THE LBP/LPS COMPLEX SEEMS

TO INTERACT WITH THE CD14 RECEPTOR.

-1- SIMILARITY: BELONGS TO THE BPI/CERP/LBP/PLTP FAMILY.

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DR EMBL: M35533; AAA59493.1; -
 DR EMBL: X98657; CAA67226.1; -
 DR EMBL: X98658; CAA67226.1; JOINED.
 DR EMBL: X98659; CAA67226.1; JOINED.
 DR EMBL: X98660; CAA67226.1; JOINED.
 DR EMBL: X98661; CAA67226.1; JOINED.
 DR EMBL: X98662; CAA67226.1; JOINED.
 DR EMBL: X98663; CAA67226.1; JOINED.
 DR EMBL: X98664; CAA67226.1; JOINED.
 DR EMBL: X98665; CAA67226.1; JOINED.
 DR EMBL: X98666; CAA67226.1; JOINED.
 DR EMBL: X98667; CAA67226.1; JOINED.
 DR EMBL: X98668; CAA67226.1; JOINED.
 DR EMBL: AF013512; AAC39547.1; -
 DR EMBL: AF013500; AAC39547.1; JOINED.
 DR EMBL: AF013501; AAC39547.1; JOINED.
 DR EMBL: AF013502; AAC39547.1; JOINED.
 DR EMBL: AF013503; AAC39547.1; JOINED.
 DR EMBL: AF013504; AAC39547.1; JOINED.
 DR EMBL: AF013505; AAC39547.1; JOINED.
 DR EMBL: AF013506; AAC39547.1; JOINED.
 DR EMBL: AF013507; AAC39547.1; JOINED.
 DR EMBL: AF013508; AAC39547.1; JOINED.
 DR EMBL: AF013509; AAC39547.1; JOINED.
 DR EMBL: AF013510; AAC39547.1; JOINED.
 DR EMBL: AF013511; AAC39547.1; JOINED.
 DR EMBL: AF105067; AAD21962.1; -
 DR EMBL: AF1080249; CAC10462.1; -
 DR EMBL: LA2172; AAA66446.1; -
 DR PIR: A35843; A35843.
 DR HSSP: P17213; 1BP1.
 DR MIM: 151990; -
 DR InterPro: IPR001124; LBP_BPI_CERP.
 DR Pfam: PF01273; LBP_BPI_CERP; 1.
 DR SMART: SM00328; LBP_BPI_CERP_C; 1.
 DR SMART: SM00329; BPI2; 1.
 DR PROSITE: PS00400; LBP_BPI_CERP; 1.
 DR Lipid transport; Antidiabetic; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 481
 FT CARBOHYD 300 300 LIPOPOLYSACCHARIDE-BINDING PROTEIN.
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 6 6 R -> H (IN REF. 2).
 FT CONFLICT 22 22 E -> C (IN REF. 2).
 FT CONFLICT 82 82 N -> K (IN REF. 4).
 FT CONFLICT 128 128 S -> F (IN REF. 4).
 FT CONFLICT 154 157 VTAS -> GYCL (IN REF. 1).
 FT CONFLICT 174 174 L -> S (IN REF. 1).
 FT CONFLICT 257 257 R -> S (IN REF. 4).
 FT CONFLICT 266 270 VMSLP -> A (IN REF. 1).
 FT CONFLICT 369 369 L -> H (IN REF. 1).
 FT CONFLICT 436 436 L -> F (IN REF. 2, 4 AND 6).
 FT SEQUENCE 481 AA; 53349 MM; 816E4B9E5E6864D0 CRC64;

Query Match 58.2%; Score 32; DB 1; Length 481;
 Best Local Similarity 62.5%; Pred. No. 63;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HOKLVFFA 9

DB 273 HNKWYFA 280

RESULT 39

CPBL_MOUSE

ID CPBL_MOUSE STANDARD; PRT; 492 AA.

AC 055071;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, last sequence update)

DT 15-DEC-1998 (Rel. 37, last annotation update)

DE Cytochrome P450 2B19 (EC 1.14.14.1) (CYP2B19).

GN CYP2B19.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=SKIN;
 RX MEDLINE=99017986; Pubmed=9799616;

RA Keeney D.S.;
 RT "The novel skin-specific cytochrome P450 Cyp2b19 maps to proximal
 RT chromosome 7 in the mouse, near a cluster of Cyp2 family genes.";
 RL Genomics 53:417-419(1998).

CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
 CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
 CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
 CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
 CC ACIDS, AND XENOBIOTICS.

CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
 CC oxidized flavoprotein + H(2)O.

CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.

CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN DIFFERENTIATED KERATINOCYTES
 CC IN SKIN.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

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DR EMBL: AF047529; AAC78770.1; -
 DR HSSP: P00178; 1DT6.
 DR MGD: MGI:107303; Cyp2b19.
 DR InterPro: IPR001128; Cyt_P450.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 DR Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Microsome; Endoplasmic reticulum; Phosphorylation.
 FT MOD_RES 129 129 PHOSPHORYLATION (BY CAPK) (BY
 FT MOD_RES 129 129 SIMILARITY).

FT BINDING 437 437 HEME (BY SIMILARITY).
 FT SEQUENCE 492 AA; 55996 MM; 9E685AF0EE2DF2A2 CRC64;

Query Match 58.2%; Score 32; DB 1; Length 492;
 Best Local Similarity 53.3%; Pred. No. 65;
 Matches 8; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 1 HOKLV-----FFA 9

DB 285 HKNWLVSVLSLFFA 299

RESULT 40

MURC_RICPR

ID MURC_RICPR STANDARD; PRT; 495 AA.

AC 092D8;

DT 30-MAY-2000 (Rel. 39, Created)

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DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
RX UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8) (UDP-N-
DE acetylmutamoyl-L-alanine synthetase).
GN MURC OR RP247.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID-782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MADRID E;
RX MEDLINE-90039499; Pubmed-9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Eliskens A.S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
CC -1- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine - ADP +
CC phosphate + UDP-N-acetylmuramoyl-L-alanine.
CC -1- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- SIMILARITY: BELONGS TO THE MURCODE FAMILY.
CC -----
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CC -----
DR EMBL: AJ235271; CAI14709.1;
DR InterPro: IPR000713; Mur_Ligase.
DR Pfam: PF01225; Mur_Ligase_1.
DR Pfam: PF02675; Mur_Ligase_C_1.
KW Peptidoglycan synthetase; Cell wall; Cell division; Ligase;
KW ATP-binding; Complete proteome.
FT NP_BIND 120 126 ATP (POTENTIAL).
SQ SEQUENCE 495 AA; 54612 MW; 2E18464088FAD2D6 CRC64;
Query Match 58.2%; Score 32; DB 1; Length 495;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 HHOKLVFFAE 10
DB 428 HHOKLVFFAE 437
RESULT 41
ACHB_MOUSE
ID ACHB_MOUSE STANDARD; PRT; 501 AA.
AC P09690;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acetylcholine receptor protein, beta chain precursor.
GN CHRM1 OR ACHR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID-10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87057335; Pubmed-3782129;
RA Buonanno A., Mudd J., Shah V., Merlie J.P.;
RT "A universal oligonucleotide probe for acetylcholine receptor genes.
RT Selection and sequencing of cDNA clones for the mouse muscle beta
RT subunit."

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RL J. Biol. Chem. 261:16451-16458(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-89214211; Pubmed-2708381;
RA Buonanno A., Mudd J., Merlie J.P.;
RT "Isolation and characterization of the beta and epsilon subunit genes
RT of mouse muscle acetylcholine receptor."
RL J. Biol. Chem. 264:7611-7616(1989).
CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -1- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC MUSCLE) CHAINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC -----
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CC -----
DR EMBL: M14537; AAA37154.1;
DR EMBL: J04699; AAA37156.1;
DR PIR: A25338; A25338.
DR MGI: 878690; Chrb1.
DR InterPro: IPR000188; GABA_A_receptor.
DR InterPro: IPR001175; Neur_channel.
DR Pfam: PF02931; Neur_chan_LBD; 1.
DR Pfam: PF02932; Neur_chan_memb; 1.
DR PRINTS: PR00252; NRIONCHANNEL.
DR PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Phosphorylation.
FT SIGNAL 1 23
FT CHAIN 24 501
FT DOMAIN 24 244
FT TRANSMEM 245 269
FT TRANSMEM 277 295
FT TRANSMEM 311 332
FT DOMAIN 333 469
FT TRANSMEM 470 488
FT DISULFID 151 165
FT CARBOHYD 164 164
FT MOD_RES 390 390
SQ SEQUENCE 501 AA; 56930 MW; 787BDDA90EB0E2 CRC64;
Query Match 58.2%; Score 32; DB 1; Length 501;
Best Local Similarity 37.5%; Pred. No. 66;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHOKLVFF 8
DB 231 HHEVITV 238
RESULT 42
ACHB_HUMAN
ID ACHB_HUMAN STANDARD; PRT; 517 AA.
AC P07510;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acetylcholine receptor protein, gamma chain precursor.
GN CHRG OR ACHRG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RX MEDLINE-85101368; PubMed-3967651;
 RA Shihabara S., Kubo T., Periski H.J., Takahashi H., Noda M., Numa S.;
 RT Cloning and sequence analysis of human genomic DNA encoding gamma
 subunit precursor of muscle acetylcholine receptor.";
 RL Eur. J. Biochem. 146:15-22(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Muscle fibroblast;
 RX MEDLINE-93345508; PubMed-7688301;
 RA Beeson D.M.W., Brydson M., Betty M., Jeremiah S., Povey S.,
 Vincent A., Newsom-Davis J.;
 RT Primary structure of the human muscle acetylcholine receptor. cDNA
 cloning of the gamma and epsilon subunits.";
 RL Eur. J. Biochem. 215:229-238(1993).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
 CC DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
 CC MUSCLE) CHAINS.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
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 CC -----
 DR EMBL: M1811; AAAS1568.2; -
 DR EMBL: L29197; AAAS1568.2; JOINED.
 DR EMBL: X01715; CAA25861.1; ALT. SEQ.
 DR EMBL: X01716; CAA25861.1; JOINED.
 DR EMBL: X01717; CAA25861.1; JOINED.
 DR EMBL: X01718; CAA25861.1; JOINED.
 DR EMBL: X01719; CAA25861.1; JOINED.
 DR EMBL: X01720; CAA25861.1; JOINED.
 DR EMBL: X01721; CAA25861.1; JOINED.
 DR EMBL: X04759; CAA25861.1; JOINED.
 DR PIR: A23261; A23261.
 DR PIR: S34776; S34776.
 DR MIM: 100730; -
 DR InterPro: IPR000188; GABA_receptor.
 DR InterPro: IPR001175; Neur_channel.
 DR Pfam: PF02931; Neur_chan_LBD; 1.
 DR Pfam: PF02932; Neur_chan Memb; 1.
 DR PRINTS: PR00252; NRIONCHANNEL.
 DR PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
 DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22
 FT CHAIN 23 517
 FT FT ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA
 FT FT CHAIN.
 FT DOMAIN 23 240
 FT TRANSMEM 241 265
 FT TRANSMEM 275 293
 FT TRANSMEM 309 330
 FT DOMAIN 331 330
 FT TRANSMEM 475 495
 FT TRANSMEM 477 497
 FT DISULFID 150 164
 FT CARBOHYD 52 52
 FT CARBOHYD 163 163
 FT SEQUENCE 517 AA; 57897 MW; D4587257087E102C CR64;
 Query Match 58.2%; Score 32; DB 1; Length 517;
 Best Local Similarity 71.4%; Pred. No. 68;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HOKUYE 8
 Db 228 HOKUYE 234
 RESULT 43
 ACHG_BOVIN
 ID ACHG_BOVIN STANDARD; PRT; 519 AA.
 AC P13536;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Acetylcholine receptor protein, gamma chain precursor.
 GN CHRG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-84285374; PubMed-6547904;
 RA Takai T., Noda M., Furutani Y., Takahashi H., Notake M., Shimizu S.,
 Kayano T., Tanabe T., Tanaka K.-I., Hirose T., Inayama S., Numa S.;
 RT Primary structure of gamma subunit precursor of calf-muscle
 acetylcholine receptor deduced from the cDNA sequence.";
 RL Eur. J. Biochem. 143:109-115(1984).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
 CC DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
 CC MUSCLE) CHAINS.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M28307; AAA30351.1; -
 DR InterPro: IPR000188; GABA_receptor.
 DR InterPro: IPR001175; Neur_channel.
 DR Pfam: PF02931; Neur_chan_LBD; 1.
 DR Pfam: PF02932; Neur_chan Memb; 1.
 DR PRINTS: PR00252; NRIONCHANNEL.
 DR PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
 DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane.
 FT SIGNAL 1 22
 FT CHAIN 23 519
 FT FT ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA
 FT FT CHAIN.
 FT DOMAIN 23 240
 FT TRANSMEM 241 265
 FT TRANSMEM 274 292
 FT TRANSMEM 308 329
 FT DOMAIN 330 476
 FT TRANSMEM 477 497
 FT TRANSMEM 477 497
 FT DISULFID 150 164
 FT CARBOHYD 52 52
 FT CARBOHYD 163 163
 FT SEQUENCE 519 AA; 58178 MW; B72DE5487E7B5C4E CR64;
 Query Match 58.2%; Score 32; DB 1; Length 519;
 Best Local Similarity 71.4%; Pred. No. 68;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 HOKLVEF 8
 Db 228 HOKVIFY 234

RESULT 44

ACHG_MOUSE STANDARD; PRT: 519 AA.
 ID ACHG_MOUSE
 AC P04760
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acetylcholine receptor protein, gamma chain precursor.
 GN CHNG OR ACHRG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66205253; PubMed=3010242;
 RA Yu L., Lapolla R.J., Davidson N.;
 RT "Mouse muscle nicotinic acetylcholine receptor gamma subunit: cDNA
 sequence and gene expression.";
 RL Nucleic Acids Res. 14:3539-3555(1986).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=66308110; PubMed=3755765;
 RA Boulter J., Evans K., Martin G., Mason P., Stengelin S.,
 RA Goldman D.J., Heinemann S.F., Patrick J.;
 RT "Isolation and sequence of cDNA clones coding for the precursor to
 the gamma subunit of mouse muscle nicotinic acetylcholine receptor.";
 RL J. Neurosci. Res. 16:37-49(1986).
 RN (3)
 RP SEQUENCE OF 1-57 FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=88108850; PubMed=3480767;
 RA Gardner P.D., Heinemann S.F., Patrick J.;
 RT "Transcriptional regulation of nicotinic acetylcholine receptor
 genes: identification of control elements of a gamma-subunit gene.";
 RL Brain Res. 427:69-76(1987).
 RN (4)
 RP SEQUENCE OF 1-18 FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=89218986; PubMed=3244354;
 RA Crowder C.M., Merlie J.P.;
 RT "Stepwise activation of the mouse acetylcholine receptor delta- and
 gamma-subunit genes in clonal cell lines.";
 RL Mol. Cell. Biol. 8:5257-5267(1988).
 RN (5)
 RP SEQUENCE OF 115-170 FROM N.A. (LONG AND SHORT FORMS).
 RX MEDLINE=95224005; PubMed=7708706;
 RA Mileo A.M., Monaco L., Palma E., Grassi F., Miledi R., Eusebi F.;
 RT "Two forms of acetylcholine receptor gamma subunit in mouse muscle.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:2686-2690(1995).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 MEMBRANE.
 CC -1- SUBUNIT: PARTNER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
 DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
 MUSCLE) CHAINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: AT LEAST IN MYOTUBES OF SKELETAL MUSCLE.
 CC -1- DEVELOPMENTAL STAGE: BOTH SHORT AND LONG ISOFORMS ARE FOUND IN A
 17 DAYS OLD EMBRYO, WHEREAS THE SHORT VARIANT IS THE ONLY ISOFORM
 PRESENT IN THE NEWBORN MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
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CC EMBL; X03818; CAA27442.1; -
 CC DR EMBL; X03819; CAA27443.1; -
 CC DR EMBL; M30514; AAB63431.1; ALT_SEQ.
 CC DR EMBL; M27455; AAA70247.1; -
 CC DR EMBL; M22381; AAA37152.1; -
 CC DR EMBL; S77465; AAB33997.2; -
 CC DR PIR; A24919; A24919.
 CC MGD; MGI:87895; Chng.
 CC DR InterPro: IPR000188; GABA_receptor.
 CC DR InterPro: IPR001175; Neur_channel.
 CC DR Pfam; PF02931; Neur_chan_LBD; 1.
 CC DR Pfam; PF02932; Neur_chan_memb; 1.
 CC DR PRINTS; PR00252; NRIONCHANNEL.
 CC DR PROSITE; PS00236; NEURON_ION_CHANNEL; 1.
 CC KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 CC Transmembrane; Alternative splicing.
 CC FT SIGNAL 1 22
 CC FT CHAIN 23 519
 CC FT DOMAIN 23 240
 CC FT TRANSMEM 241 265
 CC FT TRANSMEM 274 282
 CC FT TRANSMEM 308 329
 CC FT DOMAIN 330 476
 CC FT TRANSMEM 477 497
 CC FT DISULFID 150 164
 CC FT CARBOHYD 52 52
 CC FT CARBOHYD 153 163
 CC FT CARBOHYD 117 168
 CC FT VARSPLIC 231 231
 CC FT CONFLICT 346 346
 CC FT SEQUENCE 519 AA; 58745 MW; 3F435303564C8048 CRC64;
 CC
 CC Query Match 58.2%; Score 32; DB 1; Length 519;
 CC Best Local Similarity 71.4%; Pred. No. 68;
 CC Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 CC Oy 2 HOKLVEF 8
 CC Db 228 HOKVIFY 234
 CC
 CC RESULT 45
 CC ACHG_RAT STANDARD; PRT: 519 AA.
 CC ID ACHG_RAT
 CC AC P18916;
 CC DT 01-NOV-1990 (Rel. 16, Created)
 CC DT 01-MAY-1992 (Rel. 22, Last sequence update)
 CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
 CC DE Acetylcholine receptor protein, gamma chain precursor.
 CC GN CHNG OR ACHRG.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OX NCBI_TaxID=10116;
 CC RN (1)
 CC RP SEQUENCE FROM N.A.
 CC RX TISSUE=Muscle;
 CC MEDLINE=91093317; PubMed=1702709;
 CC Witzemann V., Stein E., Barg B., Konno T., Koenen M., Kues W.,
 CC Criado M., Hofmann M., Sakmann B.;
 CC "Primary structure and functional expression of the alpha-, beta-,
 CC gamma-, delta- and epsilon-subunits of the acetylcholine receptor
 CC from rat muscle.";
 CC Eur. J. Biochem. 194:437-448(1990).
 CC RN (2)

RP SEQUENCE OF 203-306 FROM N.A.
 RX MEDLINE-88030021: PubMed-3666131.
 RA Witzemann V., Berg B., Nishikawa Y., Sakmann B., Numa S.;
 RT "Differential regulation of muscle acetylcholine receptor gamma- and
 epsilon-subunit mRNAs.";
 RL FEBS Lett. 223:104-112(1987).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 MEMBRANE.
 CC -1- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
 DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
 MUSCLE) CHAINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
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 CC -----
 DR EMBL: X74834; CA52828.1; -;
 DR EMBL: X06364; CA29662.1; -;
 DR PIR: S03082; S03082.
 DR PIR: S13874; S13874.
 DR InterPro: IPR000188; GABA_A receptor.
 DR InterPro: IPR01175; Neur_chan.
 DR Pfam: PF02931; Neur_chan_LBD; 1.
 DR PRINTS: PR00252; Neur_chan_memb; 1.
 DR PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
 DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 transmembrane.
 KW SIGNAL
 FT CHAIN 1 22
 FT 23 519
 FT DOMAIN 23 240
 FT TRANSMEM 241 265
 FT TRANSMEM 274 292
 FT TRANSMEM 308 329
 FT DOMAIN 330 476
 FT TRANSMEM 477 497
 FT DISULFD 150 164
 FT CARBOHYD 52 52
 FT CARBOHYD 163 163
 SQ SEQUENCE 519 AA; 58621 MW; 1C97A83DE42A0D09 CRC64;
 Query Match 58.2%; Score 32; DB 1; Length 519;
 Best Local Similarity 71.4%; Pred. No. 68;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVFF 8
 DB 228 HOKLVFF 234

RESULT 46
 PRXY_ASCNO STANDARD; PRT; 557 AA.
 AC P81701;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Vanadium haloperoxidase (EC 1.11.1.-) (V-BPO).
 OS Ascomycota; stramenopiles; Phaeophyceae; Fucales; Fucaceae;
 CC Ascomycotium.
 CC NCB1_TaxID=52969;
 CC [1]
 RN SEQUENCE, X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND FUNCTION.

RX MEDLINE-20013071: PubMed-10543953;
 RA Weyand M., Hecht H.-J., Kiess M., Llaud M.-F., Vilter H.,
 RA Schomburg D.;
 RT "X-ray structure determination of a vanadium-dependent
 haloperoxidase from Ascomycotium nodosum at 2.0-A resolution.";
 RL J. Mol. Biol. 293:595-611(1999).
 CC [2]
 RN SEQUENCE OF 320-556 FROM N.A., SEQUENCE OF 326-341; 383-426; 471-479
 RP AND 481-556, AND FUNCTION.
 RX MEDLINE-96081028; PubMed-8564812;
 RA Vilter H.;
 RT "Vanadium-dependent haloperoxidases.";
 RL (Ed.) Sigel H., Sigel A. (eds.);
 RL Metal ions in biological system-vanadium and its role in life,
 RL pp. 31-325-362, Marcel Dekker, New York (1995).
 CC -1- CATALYTIC ACTIVITY: Halide + H(2)O(2) + H(+) -> HOHal + H(2)O.
 CC -1- COFACTOR: VANADIUM.
 CC -1- SUBUNIT: HOMODIMER LINKED BY TWO INTERCHAIN DISULFIDE BONDS.
 CC -1- SIMILARITY: TO OTHER BACTERIAL NON-HEME BROMO- AND CHLORO-
 PEROXIDASES.
 DR PDB: 1OI9; 1O-JUN-00.
 DR InterPro: IPR000326; PA_PTPase.
 KW Oxidoreductase; Peroxidase; Vanadium; 3D-structure.
 FT MOD_RES 1 1
 FT DISULFD 3 3
 FT DISULFD 41 41
 FT DISULFD 77 86
 FT DISULFD 441 462
 FT DISULFD 544 555
 FT ACT_SITE 411 411
 FT ACT_SITE 418 418
 FT METAL 486 486
 FT CONFLICT 321 321
 FT CONFLICT 341 341
 FT CONFLICT 403 404
 FT CONFLICT 407 408
 FT CONFLICT 409 409
 FT CONFLICT 441 444
 FT CONFLICT 470 470
 SQ SEQUENCE 557 AA; 60343 MW; E3D8557AB92B16F4 CRC64;
 Query Match 58.2%; Score 32; DB 1; Length 557;
 Best Local Similarity 66.7%; Pred. No. 73;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 HOKLVFFAE 10
 DB 507 HOKLVFFAE 515

RESULT 47
 YANG_SCHPO STANDARD; PRT; 616 AA.
 AC Q10190;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical GTP-binding protein C3F10.16C in chromosome I.
 GN SPAC3F10.16C.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 CC NCB1_TaxID=4896;
 CC [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN-972;
 RC Murphy L., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/CDJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MRL/HSR1 FAMILY OF GTP-BINDING
 PROTEINS.
 CC -----
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DR EMBL: 269369; CAA93314.1; -
 DR InterPro: IPR002917; MMR_HSR1.
 DR Pfam: PF01926; MMR_HSR1; 1.
 KW Hypothetical protein; GTP-binding.
 FT NP_BIND 308 315 GTP (POTENTIAL).
 FT NP_BIND 352 356 GTP (POTENTIAL).
 SQ SEQUENCE 616 AA; 69674 MW; F02A2996AF06FB68 CRC64;

Query Match 58.2%; Score 32; DB 1; Length 616;
 Best Local Similarity 83.3%; Pred. No. 81;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLV 6
 Db 480 HHOKIV 485

RESULT 48
 GLGB_AGRU STANDARD; PRT; 734 AA.
 ID GLGB_AGRU
 AC P52979;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Glycogen branching
 enzyme).
 GN GLGB.
 OS Agrobacterium tumefaciens.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID:358;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-A348;
 RX MEDLINE:99069330; PubMed:9851999;
 RA Ugalde J.E., Lepke V., Uttaro A.D., Estrella J., Iglesias A.,
 RA Ugalde R.A.;
 RT "Gene organization and transcription analysis of the Agrobacterium
 tumefaciens glycogen (glg) operon: two transcripts for the single
 phosphoglucomutase gene."
 RL J. Bacteriol. 180:6557-6564(1998).
 CC -1- CATALYTIC ACTIVITY: Formation of 1,6-glucosidic linkages of
 glycogen.
 CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.

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DR EMBL: AF033856; AAD03472.1; -
 DR InterPro: IPR000461; Alpha_amylase.
 DR InterPro: IPR004193; Isoamylase_N.
 DR Pfam: PF00128; alpha-amylase_N.
 DR Pfam: PF02922; Isoamylase_N; 1.
 KW Glycogen biosynthesis; Transferase; glycosyltransferase.
 FT ACT_SITE 417 417 BY SIMILARITY.
 FT ACT_SITE 470 470 BY SIMILARITY.
 FT ACT_SITE 538 538 BY SIMILARITY.
 SQ SEQUENCE 734 AA; 83623 MW; 70A3CD5A77F31E6 CRC64;

Query Match 58.2%; Score 32; DB 1; Length 734;
 Best Local Similarity 71.4%; Pred. No. 97;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLV 7
 Db 515 HHOKLV 521

RESULT 49
 PLD_PIMR STANDARD; PRT; 808 AA.
 ID PLD_PIMR
 AC 004883;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phospholipase D precursor (EC 3.1.4.4) (PLD) (Choline phosphatase)
 DE (Phosphatidylcholine-hydrolyzing phospholipase D).
 GN PLD.
 OS Pimpinella brachycarpa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids II; Apiales; Apiaceae; Pimpinella.
 OX NCBI_TaxID:45043;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Cha Y.Y., Lee K.-W., Kim J.C., Han T.J., Lee W.S., Cho S.H.;
 RT "Nucleotide sequence of a cDNA encoding phospholipase D from
 Pimpinella brachycarpa."
 RL (in) Plant Gene Register PGR97-092.
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN VARIOUS CELLULAR PROCESSES.
 CC -1- CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)O -> choline + a
 phosphatidate.
 CC -1- COFACTOR: CALCIUM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 PLDC DOMAINS.

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DR EMBL: U96438; AAB70463.1; -
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001736; PLD.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00614; PLDC; 2.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00155; PLDC; 2.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 KW Hydrolase; Lipid degradation; Calcium; Repeat.
 FT PROPEP 1 808
 FT CHAIN 1 808
 FT DOMAIN 1 109
 FT DOMAIN 326 364 C2 DOMAIN.
 FT DOMAIN 654 681 PLDC 1.
 SQ SEQUENCE 808 AA; 91672 MW; E83DA015B06F2164 CRC64;

Query Match 58.2%; Score 32; DB 1; Length 808;
 Best Local Similarity 83.3%; Pred. No. 1,1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLV 6
 Db 330 HHOKIV 335

RESULT 50

Search completed: October 29, 2002, 09:24:48
 Job time : 15 secs

```

PLD_RICCO
ID   PLD_RICCO          STANDARD;          PRT;          808 AA.
AC   041142; P93507;
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DE   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Phospholipase D precursor (EC 3.1.4.4) (PLD) (Choline phosphatase)
OS   (Phosphatidylcholine-hydrolyzing phospholipase D).
OS   Ricinus communis (Castor bean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX   NCBI_TaxID=3988;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=CV. HALE; TISSUE=Endosperm;
RX   MEDLINE=94327597; PubMed=8051126;
RA   Wang X., Xu L., Zheng L.;
RT   Cloning and expression of phosphatidylcholine-hydrolyzing
RT   phospholipase D from Ricinus communis L.;
RL   J. Biol. Chem. 269:20312-20317(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Leaf;
RX   MEDLINE=97134969; PubMed=8980529;
RA   Xu L., Zheng L., Coughlan S.J., Wang X.;
RT   Structure and analysis of phospholipase D gene from Ricinus communis
RT   L.;
RL   Plant Mol. Biol. 32:767-771(1996).
CC   -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN CELLULAR PATHWAYS INCLUDING
CC   SIGNAL TRANSDUCTION PATHWAYS.
CC   -1- CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)O -> choline + a
CC   phosphatidate.
CC   -1- COFACTOR: CALCIUM (BY SIMILARITY).
CC   -1- TISSUE SPECIFICITY: MOSTLY EXPRESSED IN VACUOLES, ENDOPLASMIC
CC   RETICULUM, A FEW IN PLASTIDS AND PLASMA MEMBRANE. EXPRESSION IS
CC   HIGHER IN RADICLE THAN IN ENDOSPERM.
CC   -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY.
CC   -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -1- SIMILARITY: CONTAINS 2 PLDC DOMAINS.
CC   -----
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CC   -----
DR   EMBL; L33686; AAB04095.1; -
DR   EMBL; U72693; AAB37305.1; -
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR001736; PLD.
DR   Pfam; PF00614; PLDC; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00155; PLDC; 2.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
KW   Hydrolyase; Lipid degradation; Calcium; Repeat.
FT   CHAIN             1..30
FT   PROPEP            1
FT   CHAIN             31..808
FT   DOMAIN            1..109
FT   DOMAIN            326..364
FT   DOMAIN            654..681
FT   CONFLICT          268
FT   CONFLICT          268
SQ   SEQUENCE 808 AA; 91992 MW; E75F6CFB9ADF3CB CRC64;

Query Match          58.2%; Score 32; DB 1; Length 808;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHOKLV 6
DB 330 HHOKIV 335

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AC 09UCA9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE BETA-AMYLLOID PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE.
RX MEDLINE-94153015; PubMed-8109908;
RA Wislowski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT "The amino acid sequence of neuritic plaque amyloid from a familial
RT Alzheimer's disease patient."
RL Ann. Neurol. 35:245-246(1994).
DR HSP; P05067; IBA4.
SQ SEQUENCE 30 AA; 3391 MW; FP4167ABD081160A CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 4; Length 30;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
DB 13 HHOKLVFAE 22

RESULT 3
ID 09UC33 PRELIMINARY; PRT; 33 AA.
AC 09UC33;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE BETA-AMYLLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE.
RX MEDLINE-93024877; PubMed-1406936;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sima S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids."
RT Nature 359:325-327(1992).
DR HSP; P05067; IBA4.
SQ SEQUENCE 33 AA; 3674 MW; B1DFE2F4167ABD0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 4; Length 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
DB 13 HHOKLVFAE 22

RESULT 4
ID P78438 PRELIMINARY; PRT; 82 AA.
AC P78438;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLLOID PROTEIN) (FRAGMENT).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID-9606;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89392030; PubMed-2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor."
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE-87120329; PubMed-2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus."
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE-93035397; PubMed-1415269;
RA Kamito K., Orr H.T., Payami H., Wajsbom E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region."
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1; -.
DR EMBL; M29269; AAA51768.1; JOINED.
DR EMBL; M15532; AAA51564.1; -.
DR EMBL; S45136; AAB23646.1; -.
DR HSP; P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
DB 29 HHOKLVFAE 38

RESULT 5
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93236601; PubMed-8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor."
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26253.2; -.
DR HSP; P05067; IBA4.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; F534A5B3EA9230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
DB 30 HHOKLVFAE 39

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RESULT 6
ID 016019 PRELIMINARY: PRT: 82 AA.
AC 016019
DT 01-NOV-1996 (TREMBLERL. 01, Created)
DT 01-NOV-1996 (TREMBLERL. 01, Last sequence update)
DE BETA-AMYLROID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor.";
RL Blochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61380; AAB26264.2; -.
DR HSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 30 HHOKLVFFAE 39

RESULT 7
ID 016020 PRELIMINARY: PRT: 82 AA.
AC 016020
DT 01-NOV-1996 (TREMBLERL. 01, Created)
DT 01-NOV-1996 (TREMBLERL. 01, Last sequence update)
DE BETA-AMYLROID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RL mutations on the processing of the beta-amyloid peptide precursor.";
RL Blochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61383; AAB26265.2; -.
DR HSP: P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8882 MW; F534AA5A5E5D9230A CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 4; Length 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 30 HHOKLVFFAE 39

RESULT 8

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013778
ID 013778 PRELIMINARY: PRT: 97 AA.
AC 013778
DT 01-NOV-1996 (TREMBLERL. 01, Created)
DT 01-NOV-1996 (TREMBLERL. 01, Last sequence update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RL brain amyloid of Alzheimer's disease.";
RL Science 235:877-880(1987).
DR EMBL: M15533; AAA35540.1; -.
DR HSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PRINTS: PR00203; AMYLOIDA4.
FT NON_TER 1
SQ SEQUENCE 97 AA; 10884 MW; E528CDBA48DE474E CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 4; Length 97;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 11 HHOKLVFFAE 20

RESULT 9
ID 093296 PRELIMINARY: PRT: 534 AA.
AC 093296
DT 01-NOV-1998 (TREMBLERL. 08, Created)
DT 01-NOV-1998 (TREMBLERL. 08, Last sequence update)
DE AMYLOID PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RL substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL: AF042098; AAC25052.1; -.
DR HSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PRINTS: PR00203; AMYLOIDA4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53BCC2E6D4C92 CRC64;

Query Match
Best Local Similarity 100.0%; Score 55; DB 13; Length 534;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 448 HHOKLVFFAE 457

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RESULT 10
Q9PVL1 PRELIMINARY; PRT; 569 AA.
ID Q9PVL1
AC Q9PVL1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RA Coulson E.J., Pallage K., Beyreuther K., Masters C.L.;
RT tells us about the evolution of the amyloid protein precursor supergene family
RL Neurochem. Int. 0:0-0(2000).
DR EMBL: AF030341; AAF12698.1; -.
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match 100.0%; Score 55; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0;

QY 1 HHOKLVEFAE 10
DB 484 HHOKLVEFAE 493

RESULT 11
Q98SGO PRELIMINARY; PRT; 693 AA.
ID Q98SGO
AC Q98SGO;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodidae; Xenopus.
OX NCBI_Taxid=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL: AJ298150; CAC37193.1; -.
DR HSSP: P05067; IBA3.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT SIGNAL 1
SQ SEQUENCE 693 AA; 78568 MW; CAFIDF655C1AB653 CRC64;

Query Match 100.0%; Score 55; DB 13; Length 693;

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Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVEFAE 10
DB 607 HHOKLVEFAE 616

RESULT 12
Q95KN7 PRELIMINARY; PRT; 695 AA.
ID Q95KN7
AC Q95KN7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_Taxid=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-CEREBELLUM;
RX MEDLINE-91273117; PubMed-1905108;
RA Podlasky M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease."
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL: M58727; AAA36829.1; -.
DR Rfam: M58727; AAA36829.1; -.
FT SIGNAL 1
FT CHAIN 597
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 100.0%; Score 55; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVEFAE 10
DB 609 HHOKLVEFAE 618

RESULT 13
Q60496 PRELIMINARY; PRT; 695 AA.
ID Q60496
AC Q60496;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_Taxid=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE-97236426; PubMed-9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing."
RL Blochim. Biophys. Acta 1351:17-21(1997).
DR EMBL: X97631; CAA66230.1; -.
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

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Query Match 100.0%; Score 55; DB 11; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
 DB 609 HHOKLVFAE 618

RESULT 14

Q9DGJ8 PRELIMINARY; PRT; 695 AA.
 AC Q9DGJ8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-AMYLROID PRECURSOR PROTEIN 695 ISOFORM.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolose A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms".
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF289218; AAG00593.1;
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 SO SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 55; DB 13; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
 DB 609 HHOKLVFAE 618

RESULT 15

Q91963 PRELIMINARY; PRT; 747 AA.
 AC Q91963;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE APP747.
 GN APP747.
 OS Xenopus.
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae.
 OX NCBI_TaxID=8353;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-93129227; PubMed-1282805;
 RA Okado H., Okamoto H.;
 RT "A Xenopus homologue of the human beta-amyloid precursor protein:
 RT developmental regulation of its gene expression".
 RL Blochman Biophys. Res. Commun. 189:1561-1568(1992).
 DR EMBL; S52417; AAB24853.1;
 DR HSSP; P05067; 1H23.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 SO SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

Query Match 100.0%; Score 55; DB 13; Length 747;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
 DB 661 HHOKLVFAE 670

RESULT 16

Q9DGJ7 PRELIMINARY; PRT; 751 AA.
 AC Q9DGJ7;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-AMYLROID PRECURSOR PROTEIN 751 ISOFORM.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolose A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 RT isoforms".
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF289219; AAG00594.1;
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00759; BASICPTASE.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 SO SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 100.0%; Score 55; DB 13; Length 751;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
 DB 665 HHOKLVFAE 674

RESULT 17

Q9TUI0 PRELIMINARY; PRT; 770 AA.
 AC Q9TUI0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE AMYLROID PRECURSOR PROTEIN.
 OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kimura A., Takahashi T.,
 RT "Amyloid Precursor Protein 770."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB035550; BAA64580.1; -
 DR HSSP; P05067; 1AAP.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOID4.
 DR PRINTS; PR00759; BASICPRASE.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Serine protease inhibitor.
 SQ SEQUENCE 770 AA; 86961 MW; 5F7ALDCB2BC583E CRC64;

Query Match 100.0%; Score 55; DB 6; Length 770;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFAE 10
 |||||
 DB 684 HHOKLVFAE 693

RESULT 18
 ID 073683 PRELIMINARY; PRT; 780 AA.
 AC 073683;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR [CONTAINS:
 DE BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].
 GN APP.
 OS Tetraodon fluviatilis (Puffer fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=47145;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 98252138; PubMed-9559080;
 RA Villard L., Tassone F., Cincogorac-Jurcevic T., Clancy K., Gardiner K.,
 RT "Analysis of pufferfish homologues of the A-beta human APP gene."
 RL Gene 210:17-24(1998).
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE
 CC BPTI/KUNITZ FAMILY OF INHIBITORS.
 DR EMBL; AF018165; AAC41275.1; -
 DR HSSP; P05067; 1H23.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.

DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOID4.
 DR PRINTS; PR00759; BASICPRASE.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; FALSE_NEG.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Serine protease inhibitor.
 SQ SEQUENCE 780 AA; 88238 MW; 60071BE94520191D CRC64;

Query Match 100.0%; Score 55; DB 13; Length 780;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFAE 10
 |||||
 DB 694 HHOKLVFAE 703

RESULT 19
 ID 098SF9 PRELIMINARY; PRT; 695 AA.
 AC 098SF9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-AMYLOID PRECURSOR PROTEIN B.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Van den Hurk W.H.;
 RL Thesis (2001), Department of Biological Sciences,
 RL University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL; AJ298151; CAC37194.1; -
 DR HSSP; P05067; 1H23.
 DR InterPro; IPR001868; A4_APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOID4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 695 AA; 78803 MW; DC14EB02AFB0204A CRC64;
 Query Match 94.5%; Score 52; DB 13; Length 695;
 Best Local Similarity 90.0%; Pred. No. 0.045;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFAE 10
 |||||
 DB 609 HHOKLVFAE 618

RESULT 20

0919E7 PRELIMINARY; PRT; 612 AA.
 AC 0919E7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE AMYLOID PROTEIN (FRAGMENT).
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Osteichthys;
 CC Cypriniformes; Cyprinidae; Danio.
 RN NCB1_TaxID=7955;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Slavov D.B., Gardiner K.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF257742; AAF71748.1;
 DR HSSP; P05067; 1H23.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS; PRO0203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR NON_TER 1
 FT 1
 SQ SEQUENCE 612 AA; 69710 MW; 59A9ACBD9C599EFF CRC64;

Query Match 89.1%; Score 49; DB 13; Length 612;
 Best Local Similarity 90.0%; Pred. No. 0.17;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFAE 10
 Db 526 YHOKLVFAE 535

RESULT 21

090W28 PRELIMINARY; PRT; 738 AA.
 AC 090W28;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE AMYLOID PRECURSOR PROTEIN.
 GN APP.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Osteichthys;
 CC Cypriniformes; Cyprinidae; Danio.
 RN NCB1_TaxID=7955;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Groch C., Lardelli M.;
 RT "Expression analysis of zebrafish app.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF389401; AAK64495.1;
 DR SEQUENCE 738 AA; 83577 MW; AF480F6D308FD298 CRC64;

Query Match 89.1%; Score 49; DB 13; Length 738;
 Best Local Similarity 90.0%; Pred. No. 0.2;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFAE 10
 Db 652 YHOKLVFAE 661

RESULT 22

033463 PRELIMINARY; PRT; 79 AA.

AC 035463;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
 GN BETA APP.
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Cricetulus.
 RN NCB1_TaxID=10029;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Sambamurti K., Pinnix I., Gandhi S.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF030413; AAB86608.1;
 DR HSSP; P05067; 1BA4.
 DR NON_TER 1
 FT 1
 SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 85.5%; Score 47; DB 11; Length 79;
 Best Local Similarity 100.0%; Pred. No. 0.053;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVFAE 10
 Db 34 HOKLVFAE 42

RESULT 23

099K32 PRELIMINARY; PRT; 607 AA.
 AC 099K32;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HYPOTHETICAL 68.4 KDA PROTEIN (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCB1_TaxID=10090;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
 RC TISSUE.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003490; AAB05490.1;
 DR HSSP; P05067; 1AAP.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PRO0203; AMYLOIDA4.
 DR PRINTS; PRO0759; BASICPTASE.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Hypothetical protein; Serine protease inhibitor.
 FT NON_TER 1
 SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 85.5%; Score 47; DB 11; Length 607;
 Best Local Similarity 100.0%; Pred. No. 0.442;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVFAE 10
 Db 522 HOKLVFAE 530


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RESULT 24
P97487
ID P97487 PRELIMINARY: PRT: 695 AA.
AC P97487; p97942;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HIPPOCAMPAL AMYLOID PROTEIN.
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SNAP8; TISSUE=HIPPOCAMPUS;
RA Flood J.F., Kumar V.B., Sasser T., Morley J.E.;
RL submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 581-662 FROM N.A.
RC STRAIN=128SV;
RA Wrigg M.A., Busfield F., Duff K., Korenblat K., Capecci M.,
RL Loring J.F., Goate A.M.;
RL submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: U84012; AAB41502.1; -
DR EMBL: U82624; AAB40919.1; -
DR HSSP: P05067; 1MMP.
DR MGD: MGI:88059; App.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOID4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78414 MW; 9A5FBE2ED261236E CRC64;

Query Match 85.5%; Score 47; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 2 HOKLVEFAE 10
|||||
Db 610 HOKLVEFAE 618

RESULT 25
057394
ID 057394 PRELIMINARY: PRT: 699 AA.
AC 057394;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE EL AMYLOID PRECURSOR PROTEIN 699.
GN EL AP699.
OS Nake japonica (Electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hyposqualae; Pristiogadidae; Batoidae;
OC Torpediniformes; Narcinoidae; Naridae; Narke.
OX NCBI_Taxid=62965;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ELECTRIC LOBE;
RA MEDLINE=98129705; PubMed=9461486;
RA Iijima K., Lee D.-S., Okutau J., Tomita S., Hirashima N., Kirino Y.,
RA Suzuki T.;
*CDNA isolation of Alzheimer's amyloid precursor protein from
cholinergic nerve terminals of the electric organ of the electric
ray.
RL Biochem. J. 330:29-33(1998).
DR EMBL: AB005544; BAA4230.1; -
DR HSSP: P05067; 1HR3
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.

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Query Match	Best Local Similarity	83.6%	Score 46;	DB 13;	Length 699;
Matches	8;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;		
QY	1 HHOKLVFF 8				
DB	613 HHOKLVFF 620				
RESULT 26					
093279	PRELIMINARY;	PRT;	737 AA.		
ID	093279				
AC	093279;				
DT	01-NOV-1998 (TREMBLrel. 08, Created)				
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN HOMOLOG PRECURSOR [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].				
DE	BETA-AMYLOID PROTEIN (BETA-APP) (A-BETA)].				
GN	App.				
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;				
OC	Tetraodontidae; Takifugu.				
OX	NCBI_TaxID=31033;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98252138; PubMed=9599080;				
RA	Villard L., Tassone F., Cnogorac-Jurcevic T., Clancy K., Gardiner K.;				
RI	"Analysis of pufferfish homologues of the At-rich human App gene.";				
RL	Gene 210:17-24(1998).				
CC	-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NKRY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE APP FAMILY.				
CC	-1- SIMILARITY: CONTAINS 1 PROTEASE INHIBITOR DOMAIN BELONGING TO THE BPT1/KUNITZ FAMILY OF INHIBITORS.				
CC	EMBL; AF090120; AAD13392.1; -				
DR	HSSP; P05067; I423.				
DR	InterPro; IPR001868; A4_APP.				
DR	InterPro; IPR002223; Kunitz_BPT1.				
DR	Pfam; PF02177; A4_EXTRA; 1.				
DR	Pfam; PF00014; Kunitz_BPT1; 1.				
DR	PRINTS; PR00203; AMYLOIDA.				
DR	PRINTS; PR00759; BASICPTASE.				
DR	SMART; SM00006; A4_EXTRA; 1.				
DR	SMART; SM00131; KU; 1.				
DR	PROSITE; PS00319; A4_EXTRA; FALSE_NEG.				
DR	PROSITE; PS00320; A4_INTRA; 1.				
DR	PROSITE; PS00280; BPT1_KUNITZ_1; 1.				
DR	PROSITE; PS00279; BPT1_KUNITZ_2; 1.				
KW	Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;				
KW	Serine protease inhibitor.				
FT	SIGNAL	1	18	POTENTIAL.	
FT	CHAIN	19	737	ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN	
FT	CHAIN	639	681	HOMOLOG.	
FT	DOMAIN	19	668	BETA-AMYLOID PROTEIN (POTENTIAL).	
FT	TRANSSEM	669	689	EXTRACELLULAR (POTENTIAL).	
FT	DOMAIN	690	737	POTENTIAL.	
FT	DOMAIN	286	344	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN	286	344	BPT1/KUNITZ INHIBITOR.	

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FT SITE 726 729 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 300 301 REACTIVE BOND.
FT DISULFID 290 340 BY SIMILARITY.
FT DISULFID 299 323 BY SIMILARITY.
FT DISULFID 315 336 BY SIMILARITY.
FT CARBOHYD 522 522 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 737 AA; 82856 MW; 6FAD01E2E3B2B7E2 CRC64;

Query Match 83.6%; Score 46; DB 13; Length 737;
Best Local Similarity 80.0%; Pred. No. 0.8;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
Db 651 YHOKLVFFAD 660

RESULT 27
O9UCC8 PRELIMINARY; PRT; 19 AA.
AC O9UCC8:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE BETA-AMYLOID-(1-42) (FRAGMENT).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE.
RA MEDLINE-94068497; PubMed-8248178;
RA Rohrer A.E., Lowenson J.D., Clarke S., Woods A.S., Cotter R.J.,
RA Cowling E., Ball M.J.;
RT "beta-Amyloid-(1-42) is a major component of cerebrovascular amyloid
RT deposits: implications for the pathology of Alzheimer disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10836-10840(1993).
DR HSP; P05067; IAMB.
SQ SEQUENCE 19 AA; 2315 MW; 05802B3F6DDECE3E CRC64;

Query Match 72.7%; Score 40; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVF 7
Db 13 HHOKLVF 19

RESULT 28
O965N2 PRELIMINARY; PRT; 1145 AA.
AC O965N2:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN BE0003M10.3.
GN BE0003M10.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA MEDLINE-99069613; PubMed-9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;

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RA Waterston R.;
RT "Direct Submission.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092690; AAK73857.1;
SQ SEQUENCE 1145 AA; 128815 MW; 67EC2437F8F4A377 CRC64;

Query Match 70.9%; Score 39; DB 5; Length 1145;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
Db 512 HHEKLIFLHE 521

RESULT 29
P96882 PRELIMINARY; PRT; 272 AA.
AC P96882:
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 30.1 KDA PROTEIN.
GN RV2277 OR MYC71.17.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_Taxid=1773;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA MEDLINE-98295987; PubMed-9634230;
RA Cole S.T., Brosch R., Parkhill J., Garrier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltham D., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne K., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
DR EMBL; Z92771; CAB07080.1;
DR Tuberculist; RV2277;
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 272 AA; 30078 MW; F07597B96A0AB081 CRC64;

Query Match 69.1%; Score 38; DB 16; Length 272;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
Db 137 HHEALLFFA 145

RESULT 30
O9K376 PRELIMINARY; PRT; 326 AA.
AC O9K376:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN PEI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-CL-3; AND DEC8B;

```

RX MEDLINE-20351039; PubMed-10894541;
 RA Reid S.D., Herbelin C.J., Bunbaugh A.C., Selander R.K., Whittam T.S.;
 "Parallel evolution of virulence in pathogenic *Escherichia coli*."
 RL Nature 406:64-67(2000).
 DR EMBL/ AF267594; AAF97134.1; -;
 DR EMBL/ AF267587; AAF97127.1; -;
 DR InterPro: IPR001672; G6P_Isomerase.
 DR Pfam: PF00342; Pgi. 1.
 DR PRINTS; PR00662; G6PISOMERASE.
 DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
 KM Isomerase.
 FT NON_TER 326 1
 SQ SEQUENCE 326 AA; 36326 MW; 326C60E6F59A625C CRC64;

Query Match 69.1%; Score 38; DB 2; Length 326;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
 DB 289 HHOKLKFPAQ 300

RESULT 31

O9K328
 ID O9K328 PRELIMINARY; PRT; 326 AA.
 AC O9K328;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
 GN Pgi.
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-921-B4, CL-37, B170, AND G5506;
 RX MEDLINE-20351039; PubMed-10894541;
 RA Reid S.D., Herbelin C.J., Bunbaugh A.C., Selander R.K., Whittam T.S.;
 "Parallel evolution of virulence in pathogenic *Escherichia coli*."
 RL Nature 406:64-67(2000).
 DR EMBL/ AF267597; AAF97137.1; -;
 DR EMBL/ AF267588; AAF97128.1; -;
 DR EMBL/ AF267592; AAF97132.1; -;
 DR EMBL/ AF267596; AAF97136.1; -;
 DR InterPro: IPR001672; G6P_Isomerase.
 DR Pfam: PF00342; Pgi. 1.
 DR PRINTS; PR00662; G6PISOMERASE.
 DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
 KM Isomerase.
 FT NON_TER 326 1
 SQ SEQUENCE 326 AA; 36333 MW; 51A210E6F59A6248 CRC64;

Query Match 69.1%; Score 38; DB 2; Length 326;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
 DB 289 HHOKLKFPAQ 300

RESULT 32

O9K273
 ID O9K273 PRELIMINARY; PRT; 326 AA.
 AC O9K273;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
 GN Pgi.
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DEC12A, AND DEC11A;
 RX MEDLINE-20351039; PubMed-10894541;
 RA Reid S.D., Herbelin C.J., Bunbaugh A.C., Selander R.K., Whittam T.S.;
 "Parallel evolution of virulence in pathogenic *Escherichia coli*."
 RL Nature 406:64-67(2000).
 DR EMBL/ AF267591; AAF97131.1; -;
 DR EMBL/ AF267590; AAF97130.1; -;
 DR InterPro: IPR001672; G6P_Isomerase.
 DR Pfam: PF00342; Pgi. 1.
 DR PRINTS; PR00662; G6PISOMERASE.
 DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
 KM Isomerase.
 FT NON_TER 326 1
 SQ SEQUENCE 326 AA; 36347 MW; AA740B3F0CF624E CRC64;

Query Match 69.1%; Score 38; DB 2; Length 326;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
 DB 289 HHOKLKFPAQ 300

RESULT 33

O9K27
 ID O9K27 PRELIMINARY; PRT; 326 AA.
 AC O9K27;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
 GN Pgi.
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DEC2A, E2348/69, AND DEC1A;
 RX MEDLINE-20351039; PubMed-10894541;
 RA Reid S.D., Herbelin C.J., Bunbaugh A.C., Selander R.K., Whittam T.S.;
 "Parallel evolution of virulence in pathogenic *Escherichia coli*."
 RL Nature 406:64-67(2000).
 DR EMBL/ AF267581; AAF97121.1; -;
 DR EMBL/ AF267579; AAF97119.1; -;
 DR EMBL/ AF267580; AAF97120.1; -;
 DR InterPro: IPR001672; G6P_Isomerase.
 DR Pfam: PF00342; Pgi. 1.
 DR PRINTS; PR00662; G6PISOMERASE.
 DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
 KM Isomerase.
 FT NON_TER 326 1
 SQ SEQUENCE 326 AA; 36400 MW; B1B240B3F0CF624E CRC64;

Query Match 69.1%; Score 38; DB 2; Length 326;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
 DB 289 HHOKLKFPAQ 300

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RESULT 34
O9K203      PRELIMINARY;      PRT;      326 AA.
AC O9K203;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN PGI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DECSD, 93-111, OK-1, DEC3F, AND 5905;
RX MEDLINE=20351039; PubMed=10894541;
RA Reid S.D., Herbelin C.J., Bumbaugh A.C., Selander R.K., Whittam T.S.;
RT "Parallel evolution of virulence in pathogenic Escherichia coli.";
RL Nature 406:64-67(2000).
DR EMBL; AF267586; AAF97126.1; -
DR EMBL; AF267582; AAF97122.1; -
DR EMBL; AF267583; AAF97123.1; -
DR EMBL; AF267584; AAF97124.1; -
DR EMBL; AF267585; AAF97125.1; -
DR InterPro: IPR001672; G6P_Isomerase.
DR Pfam: PF00342; PGI; 1.
DR PRINTS: PR00662; G6PISOMERASE.
DR PROSITE: PS00765; P_GLUCOSE_ISOMERASE_1; 1.
KW Isomerase.
FT NON_TER      1
FT TER          326
SQ SEQUENCE     326 AA; 36259 MW; BC10FCA2EFC1F7A CRC64;

Query Match
Best Local Similarity 69.1%; Score 38; DB 2; Length 326;
Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
DB 289 HHOKLSKFFAQ 300

RESULT 35
O9KH87      PRELIMINARY;      PRT;      326 AA.
AC O9KH87;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN PGI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DEC9F;
RX MEDLINE=20351039; PubMed=10894541;
RA Reid S.D., Herbelin C.J., Bumbaugh A.C., Selander R.K., Whittam T.S.;
RT "Parallel evolution of virulence in pathogenic Escherichia coli.";
RL Nature 406:64-67(2000).
DR EMBL; AF267589; AAF97129.1; -
DR InterPro: IPR001672; G6P_Isomerase.
DR Pfam: PF00342; PGI; 1.
DR PRINTS: PR00662; G6PISOMERASE.
DR PROSITE: PS00765; P_GLUCOSE_ISOMERASE_1; 1.
KW Isomerase.
FT NON_TER      1
FT TER          326
SQ SEQUENCE     326 AA; 36319 MW; 92A210FE5690515A CRC64;

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Query Match
Best Local Similarity 69.1%; Score 38; DB 2; Length 326;
Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
DB 289 HHOKLSKFFAQ 300

RESULT 36
O9KH85      PRELIMINARY;      PRT;      326 AA.
AC O9KH85;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN PGI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2FL;
RX MEDLINE=20351039; PubMed=10894541;
RA Reid S.D., Herbelin C.J., Bumbaugh A.C., Selander R.K., Whittam T.S.;
RT "Parallel evolution of virulence in pathogenic Escherichia coli.";
RL Nature 406:64-67(2000).
DR EMBL; AF267595; AAF97135.1; -
DR InterPro: IPR001672; G6P_Isomerase.
DR Pfam: PF00342; PGI; 1.
DR PRINTS: PR00662; G6PISOMERASE.
DR PROSITE: PS00765; P_GLUCOSE_ISOMERASE_1; 1.
KW Isomerase.
FT NON_TER      1
FT TER          326
SQ SEQUENCE     326 AA; 36312 MW; A905FCA2EFC1F7A CRC64;

Query Match
Best Local Similarity 69.1%; Score 38; DB 2; Length 326;
Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 HHOKLV--FFAE 10
DB 289 HHOKLSKFFAQ 300

RESULT 37
O9KH84      PRELIMINARY;      PRT;      326 AA.
AC O9KH84;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PHOSPHOGLUCOSE ISOMERASE (FRAGMENT).
GN PGI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=536;
RX MEDLINE=20351039; PubMed=10894541;
RA Reid S.D., Herbelin C.J., Bumbaugh A.C., Selander R.K., Whittam T.S.;
RT "Parallel evolution of virulence in pathogenic Escherichia coli.";
RL Nature 406:64-67(2000).
DR EMBL; AF267598; AAF97138.1; -
DR InterPro: IPR001672; G6P_Isomerase.
DR Pfam: PF00342; PGI; 1.
DR PRINTS: PR00662; G6PISOMERASE.

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DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
 RM Isomerase.
 FT NON_TER 1
 FT NON_TER 326
 SQ SEQUENCE 326 AA; 36340 MW; C76930B3P0C625A CRC64;

Query Match 69.1%; Score 38; DB 2; Length 326;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 HHOKLV--FFAE 10
 DB 289 HHOKLSKFFAQ 300

RESULT 38

Q9SN52 PRELIMINARY; PRT; 191 AA.

AC Q9SN52; PRT; 191 AA.
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE HYPOTHEMETICAL 21.7 KDA PROTEIN.
 GN F28A21.20 OR A1G18610.
 GN Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Beyan M., Mueller M.W., Muendlein A., Felber R., Bancroft I.,
 RA Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Mueller M.W., Muendlein A., Felber R., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL035526; CAB37446.1; -;
 DR EMBL; AL161549; CAB78863.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 191 AA; 21744 MW; DFB6D3495AEB132F CRC64;

Query Match 67.3%; Score 37; DB 10; Length 191;
 Best Local Similarity 60.0%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
 DB 86 HHQACVFFGQ 95

RESULT 39

Q9U0M8 PRELIMINARY; PRT; 584 AA.

AC Q9U0M8; PRT; 584 AA.
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HYPOTHEMETICAL 71.0 KDA PROTEIN.
 GN MAL1P3.09.
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 OX NCBI_TaxID=36329;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-3D7;
 RA Bowman S., Churcher C., Harris B., Harris D., Lawson D., Quail M.,
 RA Barrett B.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031746; CAB63564.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 584 AA; 70984 MW; 6E06F4C58A08F838 CRC64;

Query Match 67.3%; Score 37; DB 5; Length 584;
 Best Local Similarity 50.0%; Pred. No. 38;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
 DB 528 HHOKTVFTQ 537

RESULT 40

Q93E19 PRELIMINARY; PRT; 1035 AA.

AC Q93E19; PRT; 1035 AA.
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ADP8 RND PROTEIN.
 GN ADP8.
 OS Acinetobacter baumannii.
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
 OC Acinetobacter.
 OX NCBI_TaxID=470;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BM4454;
 RA Magnet S., Courvalin P., Lambert T.;
 RT "Characterization of a RND type efflux pump involved in aminoglycoside
 RT resistance in Acinetobacter baumannii clinical isolate";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF370885; AA14440.1; -;
 SQ SEQUENCE 1035 AA; 112614 MW; 928E7935D84BFCF3 CRC64;

Query Match 67.3%; Score 37; DB 2; Length 1035;
 Best Local Similarity 77.8%; Pred. No. 68;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HHOKLVFA 9
 DB 503 HHOKKGFFA 511

RESULT 41

Q9XST6 PRELIMINARY; PRT; 103 AA.

AC Q9XST6; PRT; 103 AA.
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE TRANSMEMBRANE PROTEIN (FRAGMENT).
 GN SAS.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-THYROID;
 RX MEDLINE-20422104; Pubmed-10964405;
 RA Pichon B., Mercan D., Pouillon V., Christophe-Hobercus C.,
 RA Christophe D.;
 RT "A method for the large-scale cloning of nuclear proteins and nuclear
 RT targeting sequences on a functional basis";
 RL Anal. Biochem. 284:231-239(2000).

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DR EMBL: AJ388529; CAB46831.1;
DR InterPro: IPR000301; Transmem_4;
DR Pfam: PF00335; transmembrane4; 1;
DR PRINTS: PR00259; TMFOUR;
FT NON_TER 103 103
SQ SEQUENCE 103 AA; 10723 MW; 5528A76F35FAC581 CRC64;

Query Match
Best Local Similarity 65.5%; Score 36; DB 6; Length 103;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVFF 8
Db 70 HHQVLEFF 77

RESULT 42
O9CUT7 PRELIMINARY; PRT; 152 AA.
ID O9CUT7
AC O9CUT7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 2700085A14RIK PROTEIN (FRAGMENT).
GN 2700085A14RIK
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=HIPPOCAMPUS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Araiawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kaubawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barbh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK013523; BAB28897.1;
DR MGD: MGI:1914375; 2700085A14RIK.
DR InterPro: IPR000301; Transmem_4.
DR PRINTS: PR00259; TMFOUR.
FT NON_TER 152 152
SQ SEQUENCE 152 AA; 16162 MW; 5815EAA2F83F1B6D CRC64;

Query Match
Best Local Similarity 65.5%; Score 36; DB 11; Length 152;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVFF 8
Db 70 HHQVLEFF 77

RESULT 43
O9CPW6 PRELIMINARY; PRT; 190 AA.
ID O9CPW6
AC O9CPW6;

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DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 2700085A14RIK PROTEIN.
GN 2700085A14RIK
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMERYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Araiawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kaubawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barbh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK012853; BAB28514.1;
DR EMBL: AK012567; BAB28322.1;
DR MGD: MGI:1914375; 2700085A14RIK.
DR InterPro: IPR000301; Transmem_4.
DR PRINTS: PR00259; TMFOUR.
SQ SEQUENCE 190 AA; 20620 MW; EFBEP9D78DACD6927 CRC64;

Query Match
Best Local Similarity 65.5%; Score 36; DB 11; Length 190;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVFF 8
Db 50 HHQVLEFF 57

RESULT 44
O9D8C2 PRELIMINARY; PRT; 204 AA.
ID O9D8C2
AC O9D8C2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE 1100001I23RIK PROTEIN.
GN 1100001I23RIK
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Araiawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kaubawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamuya M., Lee N.H.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyoko-Oka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyshav-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 DR EMBL: AK008175; BAB25510.1; -
 DR MGD: MGI:1913359; 1100001123Rik.
 DR InterPro: IPR000301; Transmem_4.
 DR Pfam: PF00335; transmembrane4; 1.
 DR PRINTS: PR00259; TMFOUR.
 SQ SEQUENCE 204 AA; 22219 MW; 76B95421EBCAE5F0 CRC64;

Query Match 65.5%; Score 36; DB 11; Length 204;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVFF 8
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 Db 70 HHQVLLFF 77

RESULT 45
 OQC088 PRELIMINARY; PRT; 210 AA.
 AC OQC088;
 RC STRAIN-C57BL/6J; TISSUE-EMBRONIC HEAD, AND EMBRYO;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyoko-Oka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyshav-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 DR EMBL: AK014183; BAB29196.1; -
 DR EMBL: AK012457; BAB28252.1; -
 DR MGD: MGI:1914375; 2700085A14Rik.
 DR InterPro: IPR000301; Transmem_4.
 DR PRINTS: PR00259; TMFOUR.
 SQ SEQUENCE 210 AA; 22694 MW; B1CAD508BEBCC9FD CRC64;

Query Match 65.5%; Score 36; DB 11; Length 210;
 Best Local Similarity 75.0%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVFF 8
 ||| |||
 Db 70 HHQVLLFF 77

RESULT 46
 OQC216 PRELIMINARY; PRT; 226 AA.
 AC OQC216;
 RC STRAIN-C57BL/6J; TISSUE-EMBRONIC HEAD, AND EMBRYO;
 RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyoko-Oka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyshav-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 DR EMBL: AK012571; BAB28326.1; -
 DR MGD: MGI:1913359; 1100001123Rik.
 DR InterPro: IPR000301; Transmem_4.
 DR Pfam: PF00335; transmembrane4; 1.
 DR PRINTS: PR00259; TMFOUR.
 SQ SEQUENCE 226 AA; 24566 MW; 684BAC91D7C42DEE CRC64;

Query Match 65.5%; Score 36; DB 11; Length 226;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOKLVFF 8
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 Db 70 HHQVLLFF 77

RESULT 47
 OQUL10 PRELIMINARY; PRT; 396 AA.
 AC OQUL10;
 RC 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DR HYPOTHETICAL 42.4 KDA PROTEIN.
 GN SARH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER.
RX MEDLINE=99375323; PubMed=10444331;
RA Eschenbrenner M., Schuman Jorns M.;
RT "Cloning and mapping of the cDNA for human sarcosine dehydrogenase, a
RL flavoenzyme defective in patients with sarcosinemia.";
EMBL: AF095737; AAD53400.2; -
DR InterPro: IPR000927; DAO.
DR InterPro: IPR000205; NAD_binding.
DR Pfam: PF01266; DAO; 1.
KW Hypothetical protein.
SQ SEQUENCE 396 AA; 42362 MW; 150CA3706476BB69 CRC64;

Query Match 65.5%; Score 36; DB 4; Length 396;
Best Local Similarity 62.5%; Pred. NO. 41;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HHOKLVFF 8
DB 348 HHTRLIF 355

RESULT 48
001165 PRELIMINARY; PRT; 535 AA.
AC 001165;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE TRANPOSASE.
OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes Incertae sedis; Magnaporthaceae; Magnaporthe.
OX NCBI_TaxID=148305;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANPOSIN-PORT;
RX MEDLINE=95115685; PubMed=7816044;
RA Kachroo P., Leong S.A., Chaitoo B.B.;
RT "Poc2, an inverted repeat transposon from the rice blast fungus
RA Magnaporthe grisea.";
RL Mol. Gen. Genet. 245:339-348(1994).
DR EMBL: Z33638; CAB83918.1; -
SQ SEQUENCE 535 AA; 61079 MW; A755F73FE6878P47 CRC64;

Query Match 65.5%; Score 36; DB 3; Length 535;
Best Local Similarity 77.8%; Pred. NO. 55;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HOKLVFFAE 10
DB 80 HOKLVFFAE 88

RESULT 49
026556 PRELIMINARY; PRT; 859 AA.
AC 026556;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-OCM-2001 (TREMblrel. 18, Last annotation update)
DE MAGNESIUM CHELATASE SUBUNIT.
GN MTH456.
OS Methanothermobacter thermoautotrophicus.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakey D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jivani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RL deltaH: functional analysis and comparative genomics.";
EMBL: AE000830; AAB84962.1; -
DR InterPro: IPR003672; COBN/Mg_chel.
DR Pfam: PF02514; COBN-Mg_chel; 1.
KW Complete proteome.
SQ SEQUENCE 859 AA; 97572 MW; 0C7946B7839EF5ED CRC64;

Query Match 65.5%; Score 36; DB 17; Length 859;
Best Local Similarity 66.7%; Pred. NO. 89;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
DB 210 HHQYLAFFA 218

RESULT 50
027011 PRELIMINARY; PRT; 1668 AA.
AC 027011;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-OCM-2001 (TREMblrel. 18, Last annotation update)
DE COBALAMIN BIOSYNTHESIS PROTEIN N.
GN MTH928.
OS Methanothermobacter thermoautotrophicus.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakey D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jivani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RL deltaH: functional analysis and comparative genomics.";
EMBL: AE000830; AAB84962.1; -
DR InterPro: IPR003672; COBN/Mg_chel.
DR Pfam: PF02514; COBN-Mg_chel; 1.
KW Complete proteome.
SQ SEQUENCE 1668 AA; 184731 MW; 73D53E89519EAC00 CRC64;

Query Match 65.5%; Score 36; DB 17; Length 1668;
Best Local Similarity 66.7%; Pred. NO. 17+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
DB 792 HHQYLAFFA 800

Search completed: October 29, 2002, 09:25:20
Job time : 28 secs

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3	42	76.4	8	4	US-08-703-675C-28	Sequence 28	App
4	42	76.4	8	4	US-08-617-267C-5	Sequence 5	App1
5	38	69.1	7	2	US-08-612-785B-6	Sequence 6	App1
6	38	69.1	7	4	US-08-703-675C-29	Sequence 29	App
7	38	69.1	7	4	US-08-617-267C-6	Sequence 6	App1
8	34	61.8	7	1	US-08-127-904-14	Sequence 14	App
9	34	61.8	7	1	US-08-397-633A-105	Sequence 105	App
10	34	61.8	7	2	US-08-612-785B-7	Sequence 7	App1
11	34	61.8	7	4	US-08-703-675C-30	Sequence 30	App
12	34	61.8	7	4	US-08-617-267C-7	Sequence 7	App1
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17	34	61.8	10	5	US-08-970-833-3	Sequence 3	App1
18	30	54.5	6	2	US-08-612-785B-8	Sequence 8	App1
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21	30	54.5	6	4	US-09-242-724-24	Sequence 24	App1
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23	30	54.5	6	4	US-08-723-661B-3	Sequence 3	App1
24	29	52.7	6	2	US-08-612-785B-9	Sequence 9	App1
25	29	52.7	6	4	US-08-612-785B-27	Sequence 27	App
26	29	52.7	6	4	US-08-703-675C-32	Sequence 32	App
27	29	52.7	6	4	US-08-703-675C-40	Sequence 40	App

28	29	52.7	6	4	US-08-617-267C-9	Sequence 9, App1
29	29	52.7	6	4	US-08-617-267C-9	Sequence 27, App
30	27	49.1	6	4	US-09-242-724-27	Sequence 27, App
31	27	49.1	6	4	US-09-242-724-27	Sequence 30, App
32	26	47.3	4	3	US-08-717-551A-1	Sequence 1, App1
33	26	47.3	6	4	US-09-242-724-33	Sequence 33, App
34	25	45.5	5	1	US-08-127-904-15	Sequence 15, App
35	25	45.5	5	2	US-08-612-785B-10	Sequence 10, App
36	25	45.5	5	3	US-08-970-833-2	Sequence 2, App1
37	25	45.5	5	4	US-08-703-675C-6	Sequence 46, App1
38	25	45.5	5	4	US-09-242-724-25	Sequence 25, App
39	25	45.5	5	4	US-09-242-724-25	Sequence 26, App
40	25	45.5	5	4	US-08-617-267C-10	Sequence 10, App
41	25	45.5	5	4	US-08-617-267C-10	Sequence 28, App
42	25	45.5	5	5	US-09-264-705A-28	Sequence 15, App1
43	25	45.5	5	5	PCR-US94-10475-15	Sequence 28, App
44	25	45.5	6	2	US-08-612-785B-11	Sequence 31, App
45	25	45.5	6	3	US-08-664-370B-19	Sequence 19, App
46	25	45.5	6	4	US-08-703-675C-44	Sequence 44, App
47	25	45.5	6	4	US-09-242-724-31	Sequence 31, App
48	25	45.5	6	4	US-08-617-267C-31	Sequence 31, App
49	25	45.5	8	4	US-08-617-267C-43	Sequence 43, App
50	24	43.6	5	2	US-08-970-833-4	Sequence 4, App1
					US-08-612-785B-11	Sequence 11, App

ALIGNMENTS

```

RESULT 1
US-09-264-709A-4
: Sequence 4, Application US/09264709A
: Patent No. 6320024
: GENERAL INFORMATION:
: APPLICANT: Roberts, Eugene
: TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
: TITLE OF INVENTION: Improve the Quality of Life
: FILE REFERENCE: 2124-310
: CURRENT APPLICATION NUMBER: US/09/264,709A
: PRIOR APPLICATION NUMBER: 08/797,782
: PRIOR FILING DATE: 1997-02-07
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 4
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-264-709A-4

Query Match
Best Local Similarity 83.6%; Score 46; DB 4; Length 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HNKIYFF 8
|||||
Db 2 HNKIYFF 9

RESULT 2
US-08-612-785B-5
: Sequence 5, Application US/08612785B
: Patent No. 5854204
: GENERAL INFORMATION:
: APPLICANT: Findels, Mark A. et al.
: TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
: TITLE OF INVENTION: Aggregation
: NUMBER OF SEQUENCES: 40
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 28 State Street, Suite 510
: City: Boston
: STATE: Massachusetts
: COUNTRY: USA

```

ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Decontl, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPT-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-785B-5

Query Match 76.4%; Score 42; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HOKLVEFA 9
DB 1 HOKLVEFA 8

RESULT 3
US-08-703-675C-28
Sequence 28, Application US/08703675C
Patent No. 630367
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995

Aggregation Comprising D-

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPT-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-28

Query Match 76.4%; Score 42; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HOKLVEFA 9
DB 1 HOKLVEFA 8

RESULT 4
US-08-617-267C-5
Sequence 5, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Decontl, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPT-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-5

Query Match 76.4%; Score 42; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVFFA 9
Db 1 HOKLVFFA 8

RESULT 5
US-08-612-785B-6
Sequence 6, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that modulate b-Amyloid
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-785B-6

Query Match 69.1%; Score 38; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVFF 8
Db 1 HOKLVFF 7

RESULT 6
US-08-703-675C-29

Sequence 29, Application US/08703675C
Patent No. 6303567
GENERAL INFORMATION:

APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-29

Query Match 69.1%; Score 38; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOKLVFF 8
Db 1 HOKLVFF 7

RESULT 7
US-08-617-267C-6
Sequence 6, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-6

Query Match 69.1%; Score 38; DB 4; Length 7;
Best local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 2 HOKLVEF 8
DB 1 HOKLVEF 7

RESULT 8
US-08-127-904-14
Sequence 14, Application US/08127904
Patent No. 5470951
GENERAL INFORMATION:
APPLICANT: Eugene Roberts
TITLE OF INVENTION: Method For Antagonizing
TITLE OF INVENTION: Amesetic Effects of Amyloid n
TITLE OF INVENTION: Protein and Improving the
TITLE OF INVENTION: Quality of Life in Individuals
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: City of Hope
STREET: 1500 East Duarte Road
CITY: Duarte
STATE: California
COUNTRY: United States of America
ZIP: 91010-0269
COMPUTER READABLE FORM:
MEDIUM TYPE: 3M Double Density 5 1/4" diskette
COMPUTER: Wang PC
OPERATING SYSTEM: MS DOS Version 3.20
SOFTWARE: Microsoft
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,904
FILING DATE: 29 September 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA: No. 5470951e
ATTORNEY/AGENT INFORMATION:
NAME: Itons, Edward S.
REGISTRATION NUMBER: 16,541

REFERENCE/DOCKET NUMBER: No. 5470951e
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
TELEX: No. 5470951e
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7
TYPE: Amino Acid
STRANDEDNESS:
TOPOLOGY: Unknown
US-08-127-904-14

Query Match 61.8%; Score 34; DB 1; Length 7;
Best local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0;

QY 4 KLVFAE 10
DB 1 KLVFAE 7

RESULT 9
US-08-397-633A-105
Sequence 105, Application US/08397633A
Patent No. 5773577
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
TITLE OF INVENTION: OF ENZYMAITC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertlam I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-633A-105

Query Match 61.8%; Score 34; DB 1; Length 7;
Best local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 1 HHOKIV 6
DB 2 HHOKIV 7

RESULT 10
US-08-612-785B-7
Sequence 7, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-785B-7

Query Match 61.8%; Score 34; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 OKLVFFA 9
Db 1 OKLVFFA 7

RESULT 11
US-08-703-675C-30
Sequence 30, Application US/08703675C
Patent No. 6303567
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

Aggregation Comprising D-

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-30

Query Match 61.8%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 OKLVFFA 9
Db 1 OKLVFFA 7

RESULT 12
US-08-617-267C-7
Sequence 7, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579

;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA: USSN 08/548,998
;; APPLICATION NUMBER: 27-OCT-1995
;; FILING DATE: 27-OCT-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeConti, Giulio A.
;; REGISTRATION NUMBER: 31,503
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)227-5941
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-617-267C-7

Query Match 61.8%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KLVFFA 9
Db 1 KLVFFA 7

RESULT 13
US-09-264-709A-13
;; Sequence 13, Application US/09264709A
;; Patent No. 6320024
;; GENERAL INFORMATION:
;; APPLICANT: Roberts, Eugene
;; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
;; FILE REFERENCE: 2124-310
;; CURRENT APPLICATION NUMBER: US/09/264,709A
;; PRIOR FILING DATE: 1999-03-09
;; PRIOR APPLICATION NUMBER: 08/797,782
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 13
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-264-709A-13

Query Match 61.8%; Score 34; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLVFFAE 10
Db 1 KLVFFAE 7

RESULT 14
PCT-US94-10475-14
;; Sequence 14, Application PC/TUS9410475
;; GENERAL INFORMATION:
;; APPLICANT: Eugene Roberts
;; TITLE OF INVENTION: Method For
;; TITLE OF INVENTION: Antagonizing Amnesic
;; TITLE OF INVENTION: Effects of Amyloid n
;; TITLE OF INVENTION: Protein and Improving
;; TITLE OF INVENTION: the Quality of Life
;; TITLE OF INVENTION: in Individuals
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESS: City of Hope

;; STREET: 1500 East Duarte Road
;; CITY: Duarte
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 91010-0269
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3M Double Density 5 1/4"
;; MEDIUM TYPE: diskette
;; COMPUTER: Wang PC
;; OPERATING SYSTEM: MS DOS Version 3.20
;; SOFTWARE: Microsoft
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/10475
;; FILING DATE: 16 September 1994
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA: U. S. Application
;; PRIOR APPLICATION DATA: Serial No.
;; PRIOR APPLICATION DATA: 08/127,904; filed
;; PRIOR APPLICATION DATA: 29 September 1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Itons, Edward S.
;; REGISTRATION NUMBER: 16,541
;; REFERENCE//DOCKET NUMBER: None
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 626-3564 or 783-6030
;; TELEFAX: (202) 783-6031
;; TELEX: None
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7
;; TYPE: Amino Acid
;; STRANDEDNESS:
;; TOPOLOGY: Unknown
PCT-US94-10475-14

Query Match 61.8%; Score 34; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLVFFAE 10
Db 1 KLVFFAE 7

RESULT 15
US-08-630-645-1
;; Sequence 1, Application US/08630645
;; Patent No. 5948763
;; GENERAL INFORMATION:
;; APPLICANT: SOTO-JARA, Claudio
;; APPLICANT: BAUMANN, Marc
;; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
;; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
;; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 400
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/630,645
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-630-645-1

Query Match 61.8%; Score 34; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFFAE 10
|||||
DB 1 KLVFFAE 7

RESULT 16
PCT-US96-10220-1
Sequence 1, Application PC/TUS9610220
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10220
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-10220-1

Query Match 61.8%; Score 34; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFFAE 10
|||||
DB 1 KLVFFAE 7

RESULT 17
US-08-970-833-3
Sequence 3, Application US/08970833
Patent No. 6022859
GENERAL INFORMATION:
APPLICANT: Klessling, Laura L.
APPLICANT: Murphy, Regina M.
TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,833
FILING DATE:
CLASSIFICATION: .530
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 960296.94291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
TELEFAX: (414) 271-3552
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-970-833-3

Query Match 61.8%; Score 34; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFFAE 10
|||||
DB 1 KLVFFAE 7

RESULT 18
US-08-612-785B-8
Sequence 8, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: AD peptides that modulate b-Amyloid
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts

COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Decont, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-785B-8

Query Match 54.5%; Score 30; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 OKLVFF 8
Db 1 OKLVFF 6

RESULT 19
US-08-461-216-3
Sequence 3, Application US/08461216
Patent No. 5938883
GENERAL INFORMATION:
APPLICANT: Snow, A.D.
TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,216
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,734
FILING DATE: October 23, 1992
APPLICATION NUMBER: 07/950,417
FILING DATE: September 23, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: UOFW-1-6707
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
TELEFAX: 1-206-224-0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: [SYMBOL 98 \f "Symbol"]/A4(12-17);
DESCRIPTION: page 60, line 4-5; page 83, line 33 and 27-28
US-08-461-216-3

Query Match 54.5%; Score 30; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKL 5
Db 2 HHOKL 6

RESULT 20
US-08-703-675C-31
Sequence 31, Application US/08703675C
Patent No. 6303567
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-31

Query Match
Best Local Similarity 54.5%; Score 30; DB 4; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 OKLVEF 8
DB 1 OKLVEF 6

RESULT 21
US-09-242-724-24
Sequence 24, Application US/09242724
Patent No. 6316405

GENERAL INFORMATION:
APPLICANT: Solomon, Michael E.
APPLICANT: Rich, Daniel H.
TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
FILE REFERENCE: Cyclosporin Analogs
CURRENT APPLICATION NUMBER: US/09/242,724
CURRENT FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-242-724-24

Query Match
Best Local Similarity 54.5%; Score 30; DB 4; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 OKLVEF 8
DB 1 OKLVEF 6

RESULT 22
US-08-617-267C-8

Sequence 8, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579

FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Decontt, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-8

Query Match
Best Local Similarity 54.5%; Score 30; DB 4; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 OKLVEF 8
DB 1 OKLVEF 6

RESULT 23
US-08-723-661B-3
Sequence 3, Application US/08723661B
Patent No. 6340783

GENERAL INFORMATION:
APPLICANT: Alan D Snow
TITLE OF INVENTION: Animal Models of Human Amyloidosis
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrick M. Dwyer
STREET: 1818 Westlake Avenue N, Suite 114
CITY: Seattle
STATE: WA (Washington)
COUNTRY: United States of America
ZIP: 98109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage

OPERATING SYSTEM: IBM PC

SOFTWARE: WordPerfect 5.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/723,661B

FILING DATE: 31-Oct-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/461,216

FILING DATE: 05-Jun-1995

APPLICATION NUMBER: 07/969,734

FILING DATE: 23-Oct-1992

APPLICATION NUMBER: 07/950,417

FILING DATE: 23-Sep-1992

ATTORNEY/AGENT INFORMATION:

NAME: Dwyer, Patrick M.

REGISTRATION NUMBER: 32,411

REFERENCE/DOCKET NUMBER: PROTEO.P00C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 343-7074

TELEFAX: (206) 343-7085

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: PEPTIDE

DESCRIPTION: /A4 (12-17); page 60, lines 4-5; page 83,

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-723-661B-3

Query Match 54.5%; Score 30; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKL 5
| | | | |
DB 2 HHOKL 6

RESULT 24

US-08-612-785B-9
; Sequence 9, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Ab peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-9

Query Match 52.7%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFFA 9
| | | | |
DB 1 KLVFFA 6

RESULT 25

US-08-612-785B-27
; Sequence 27, Application US/08612785B

; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Ab peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-27

Query Match 52.7%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LVFFAE 10
| | | | |
DB 1 LVFFAE 6

RESULT 26

US-08-703-675C-32
; Sequence 32, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide Aggregation Comprising
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; SOFTWARE: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-32

Query Match 52.7%; Score 29; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LKVEFA 9
|||||
Db 1 LKVEFA 6

RESULT 27
US-08-703-675C-40
Sequence 40, Application US/08703675C
Patent No. 6303567
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-40

Query Match 52.7%; Score 29; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LKVEFAE 10
|||||
Db 1 LKVEFAE 6

RESULT 28
US-08-617-267C-9
Sequence 9, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHYE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Decouti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-617-267C-9

Query Match 52.7%; Score 29; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFFA 9
DB 1 KLVFFA 6

RESULT 29

US-08-617-267C-27
Sequence 27, Application US/08617267C
Patent No. 6319498

GENERAL INFORMATION:
APPLICANT: FINEDEL, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Decont, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-27

Query Match 52.7%; Score 29; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LVFFAE 10
DB 1 LVFFAE 6

RESULT 30
US-09-242-724-27
Sequence 27, Application US/09242724
Patent No. 6316405
GENERAL INFORMATION:

APPLICANT: SOLOMON, Michael E.
APPLICANT: Rich, Daniel H.
TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
FILE REFERENCE: Cyclosporin Analogs
CURRENT APPLICATION NUMBER: US/09/242,724
CURRENT FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: polypeptide
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
NAME/KEY: MOD_RES
LOCATION: (2)
OTHER INFORMATION: K(2Cl-Cbz) - 2-chlorobenzylloxycarbonyl-protected
OTHER INFORMATION: Lysine
US-09-242-724-27

Query Match 49.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 OKLVFF 8
DB 1 KLVFF 6

RESULT 31
US-09-242-724-30
Sequence 30, Application US/09242724
Patent No. 6316405
GENERAL INFORMATION:
APPLICANT: SOLOMON, Michael E.
APPLICANT: Rich, Daniel H.
TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
FILE REFERENCE: Cyclosporin Analogs
CURRENT APPLICATION NUMBER: US/09/242,724
CURRENT FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: polypeptide
US-09-242-724-30

Query Match 49.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 OKLVFF 8
DB 1 KLVFF 6

RESULT 32
US-08-717-551A-1
Sequence 1, Application US/08717551A
Patent No. 6071493
GENERAL INFORMATION:
APPLICANT: Dana Gullian
TITLE OF INVENTION: Identification of Agents that Protect
TITLE OF INVENTION: Against Inflammatory Injury to Neurons
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: 6 NO. 6071493rls LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT FOR WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,551A
FILING DATE: Sept-20-96
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-717-551A-1

Query Match 47.3%; Score 26; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOK 4
Db 1 HHOK 4

RESULT 33
US-09-242-724-33
Sequence 33, Application US/09242724
Patent No. 6316405
GENERAL INFORMATION:
APPLICANT: Solomon, Michael E.
APPLICANT: Rich, Daniel H.
TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
FILE REFERENCE: Cyclosporin Analogs
CURRENT APPLICATION NUMBER: US/09/242,724
CURRENT FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: polypeptide
US-09-242-724-33

Query Match 47.3%; Score 26; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OKLVFF 8
Db 1 KLVFF 6

RESULT 34
US-08-127-904-15
Sequence 15, Application US/08127904
Patent No. 5470951
GENERAL INFORMATION:
APPLICANT: Eugene Roberts
TITLE OF INVENTION: Method For Antagonizing
TITLE OF INVENTION: Amnesic Effects of Amyloid n
TITLE OF INVENTION: Protein and Improving the
TITLE OF INVENTION: Quality of Life in Individuals
TITLE OF INVENTION: With Alzheimer Disease
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: City of Hope
STREET: 1500 East Duarte Road
CITY: Duarte
STATE: California
COUNTRY: United States of America
ZIP: 91010-0269

COMPUTER READABLE FORM:
MEDIUM TYPE: 3M Double Density 5 1/4" diskette
COMPUTER: Wang PC
OPERATING SYSTEM: MS DOS Version 3.20
SOFTWARE: Microsoft
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,904
FILING DATE: 29 September 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA: No. 5470951e
ATTORNEY/AGENT INFORMATION:
NAME: Irons, Edward S.
REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: No. 5470951e
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
TELEX: No. 5470951e
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 5
TYPE: Amino Acid
STRANDEDNESS:
TOPOLOGY: Unknown
US-08-127-904-15

Query Match 45.5%; Score 25; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLVFF 8
Db 1 KLVFF 5

RESULT 35
US-08-612-785B-10
Sequence 10, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-785b-10

Query Match 45.5%; Score 25; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFF 8
1 KLVFF 5

RESULT 36
US-08-970-833-2
Sequence 2, Application US/08970833
Patent No. 6022859
GENERAL INFORMATION:
APPLICANT: Klessling, Laura L.
APPLICANT: Murphy, Regina M.
TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/970,833
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 960296,94291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5709
TELEFAX: (414) 271-3552

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-970-833-2

Query Match 45.5%; Score 25; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFF 8
1 KLVFF 5

RESULT 37
US-08-703-675C-46
Sequence 46, Application US/08703675C
Patent No. 6303567
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kere, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-46

Query Match 45.5%; Score 25; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLVFF 8
1 KLVFF 5

RESULT 38
US-09-242-724-25
Sequence 25, Application US/09242724
Patent No. 6316405
GENERAL INFORMATION:
APPLICANT: Solomon, Michael E.
APPLICANT: Rich, Daniel H.
TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
FILE REFERENCE: Cyclosporin Analogs
CURRENT APPLICATION NUMBER: US/09/242,724
CURRENT FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: :
US-09-242-724-25

Query Match 45.5%; Score 25; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLVFF 8
1 KLVFF 5

RESULT 39
US-09-242-724-26
Sequence 26, Application US/09242724
Patent No. 6316405
GENERAL INFORMATION:
APPLICANT: Solomon, Michael E.
APPLICANT: Rich, Daniel H.
TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
FILE REFERENCE: Cyclosporin Analogs
CURRENT APPLICATION NUMBER: US/09/242,724
CURRENT FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLTATION: R(2C1-CH2) -
OTHER INFORMATION: 2-chlorobenzylloxycarbonyl-protected lysine
US-09-242-724-26

Query Match 45.5%; Score 25; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLVFF 8
1 KLVFF 5

RESULT 40
US-08-617-267C-10
Sequence 10, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Flindels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Decortli, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPT-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-10

OY 4 KLVFF 8
1 KLVFF 5

Query Match 45.5%; Score 25; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLVFF 8
1 KLVFF 5

RESULT 41
US-09-264-709A-28
Sequence 28, Application US/09264709A
Patent No. 6320024
GENERAL INFORMATION:
APPLICANT: Roberts, Eugene
TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
FILE REFERENCE: 2124-310
CURRENT APPLICATION NUMBER: US/09/264,709A
CURRENT FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: 08/797,782
PRIOR FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: memory-modulating peptide

US-09-264-709A-28

Query Match 45.5%; Score 25; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VFPAE 10
11111
Db 1 VFPAE 5

RESULT 42

PCT-US94-10475-15
Sequence 15, Application PC/TUS9410475
GENERAL INFORMATION:
APPLICANT: Eugene Roberts
TITLE OF INVENTION: Method For
TITLE OF INVENTION: Antagonizing Amyloid n
TITLE OF INVENTION: Effects of Amyloid n
TITLE OF INVENTION: Protein and Improving
TITLE OF INVENTION: the Quality of Life
TITLE OF INVENTION: In Individuals
TITLE OF INVENTION: With Alzheimer Disease
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: City of Hope
STREET: 1500 East Duarte Road
CITY: Duarte
STATE: California
COUNTRY: United States of America
ZIP: 91010-0269
COMPUTER READABLE FORM:
MEDIUM TYPE: 3M Double Density 5 1/4"
MEDIUM TYPE: diskette
COMPUTER: Wang PC
OPERATING SYSTEM: MS DOS Version 3.20
SOFTWARE: Microsoft
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10475
FILING DATE: 16 September 1994
CLASSIFICATION:
PRIOR APPLICATION DATA: U. S. Application
PRIOR APPLICATION DATA: Serial No.
PRIOR APPLICATION DATA: 08/127,904; filed
PRIOR APPLICATION DATA: 29 September 1993
ATTORNEY/AGENT INFORMATION:
NAME: Irons, Edward S.
REGISTRATION NUMBER: 16,541
REFERENCE/DOCKET NUMBER: None
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 626-3564 or 783-6030
TELEFAX: (202) 783-6031
TELEX: None
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 5
TYPE: Amino Acid
STRANDEDNESS:
TOPOLOGY: Unknown
PCT-US94-10475-15

Query Match 45.5%; Score 25; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFF 8
11111
Db 1 KLVFF 5

RESULT 43

US-08-612-785B-31
Sequence 31, Application US/08612785B

Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 6
OTHER INFORMATION: /note= Xaa is beta-alanyl

US-08-612-785B-31

Query Match 45.5%; Score 25; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFF 8
11111
Db 1 KLVFF 5

RESULT 44

US-08-664-379B-19
Sequence 19, Application US/08664379B
Patent No. 6034211
GENERAL INFORMATION:
APPLICANT: Kelly, Jeffery W.
TITLE OF INVENTION: BETA-SHEET NUCLEATING PEPTIDOMIMETICS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: U.S.A.

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,379B
FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/018,925
FILING DATE: 03-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 08435/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
LOCATION: 1..1
OTHER INFORMATION: wherein Xaa at position 1 is Ornithine
US-08-664-379B-19

Query Match 45.5%; Score 25; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFF 8
|||||
DB 2 KLVFF 6

RESULT 45
US-08-703-675C-44
Sequence 44, Application US/08703675C
Patent No. 6303567
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of -Amyloid peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995

Aggregation comprising D-

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 6
OTHER INFORMATION: /note= Xaa is beta-alanyl
US-08-703-675C-44

Query Match 45.5%; Score 25; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFF 8
|||||
DB 1 KLVFF 5

RESULT 46
US-09-242-724-31
Sequence 31, Application US/09242724
Patent No. 6316405
GENERAL INFORMATION:
APPLICANT: Solomon, Michael E.
TITLE OF INVENTION: Cyclosporin A Conjugates and Uses Therefor
FILE REFERENCE: Cyclosporin Analogs
CURRENT APPLICATION NUMBER: US/09/242,724
CURRENT FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 6
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-242-724-31

Query Match 45.5%; Score 25; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLVFF 8
|||||
DB 1 KLVFF 5

RESULT 47
US-08-617-267C-31
Sequence 31, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street

CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Decontl, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 6
OTHER INFORMATION: /note= Xaa is beta-alanyl
US-08-617-267C-31
Query Match 45.5%; Score 25; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 KLVFF 8
DB 1 KLVFF 5
RESULT 48
US-08-617-267C-43
Sequence 43, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Decontl, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-617-267C-43
Query Match 45.5%; Score 25; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 KLVFF 8
DB 2 KLVFF 6

RESULT 49
US-08-970-833-4
Sequence 4, Application US/08970833
Patent No. 6022859
GENERAL INFORMATION:
APPLICANT: Riessling, Laura L.
TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/970,833
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 960296.94291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 271-3552
TELEFAX: (414) 271-3552
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-970-833-4

Query Match 45.5%; Score 25; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 6 VFFAE 10
1 VFFAE 5

RESULT 50
US-08-612-785B-11

; Sequence 11, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Fintel, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHYE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-612-785B-11

Query Match 43.6%; Score 24; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 5 LVFFA 9
1 LVFFA 5

Search completed: October 29, 2002, 09:39:08
Job time : 14 secs

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OM protein - protein search, using sw model

Run on: October 29, 2002, 09:35:42 ; Search time 14 Seconds

(without alignments)
68.635 Million cell updates/sec

Title: US-09-724-842a-27

Perfect score: 55

Sequence: 1 HHQKLVFPAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1099

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	36.4	5	2	C41225	Copper resistance
2	20	36.4	9	2	PT0080	60K Ca binding pro
3	18	32.7	10	2	S65387	cytochrome-c oxida
4	16	29.1	6	2	A46474	EC epsilon R11b -
5	16	29.1	9	2	S13889	phosphoenolpyruvat
6	15	27.3	10	2	S74176	glucosyltransferase
7	15	27.3	8	2	S21273	cellulase (EC 3.2.
8	15	27.3	9	2	A61102	parathyroid hormon
9	15	27.3	9	2	T31612	hypothetical prote
10	15	27.3	9	2	S10920	venom protein HR-3
11	15	27.3	9	2	B39504	octamer-binding pr
12	15	27.3	10	2	PT0310	Ig heavy chain CRD
13	15	27.3	10	2	PT0807	T-cell receptor al
14	15	25.5	7	2	A30812	sex pheromone cCf1
15	14	25.5	9	2	B20569	serum amyloid P-co
16	14	25.5	10	2	PH0113	alpha-amylase (EC
17	14	25.5	10	2	S43631	cytochrome-c oxida
18	13	23.6	4	2	T46627	hypothetical prote
19	13	23.6	6	2	S71349	beta-crystallin B2
20	13	23.6	8	2	PT0368	Ig gamma chain C r
21	13	23.6	9	2	S55696	phosphoenolpyruvat
22	13	23.6	10	2	S65388	cytochrome-c oxida
23	13	23.6	10	2	S30348	clotting protein -
24	13	23.6	10	2	S43625	cytochrome-c oxida
25	13	23.6	10	2	PT0284	Ig heavy chain CRD
26	13	23.6	10	2	B45482	platelet activatin
27	13	23.6	10	2	T13838	cytochrome-c oxida
28	13	23.6	10	2	T13976	cytochrome-c oxida
29	13	23.6	10	2	T17057	cytochrome-c oxida

30	13	23.6	10	2	T12303	cytochrome-c oxida
31	13	23.6	10	2	T14019	cytochrome-c oxida
32	13	23.6	10	2	T17060	cytochrome-c oxida
33	13	23.6	10	2	T14043	cytochrome-c oxida
34	13	23.6	10	2	T14054	cytochrome-c oxida
35	13	23.6	10	2	T17066	cytochrome-c oxida
36	13	23.6	10	2	T17069	cytochrome-c oxida
37	13	23.6	10	2	T12308	cytochrome-c oxida
38	13	23.6	10	2	T17072	cytochrome-c oxida
39	13	23.6	10	2	T12312	cytochrome-c oxida
40	13	23.6	10	2	T12316	cytochrome-c oxida
41	13	23.6	10	2	T12321	cytochrome-c oxida
42	13	23.6	10	2	T14219	cytochrome-c oxida
43	12	21.8	4	2	J01273	neuropeptide Antho
44	12	21.8	4	2	A32480	achatin-I - giant
45	12	21.8	6	2	A60986	N-formyl oligopept
46	12	21.8	6	2	TS9142	platelet-derived g
47	12	21.8	6	2	A43129	neuropeptide GnFR
48	12	21.8	7	2	PT0246	Ig heavy chain CRD
49	12	21.8	7	2	I46868	alpha-myosin heavy
50	12	21.8	8	2	T13818	cytochrome oxidase

ALIGNMENTS

RESULT 1
C41225
Copper resistance protein - Pseudomonas syringae pv. tomato (fragment)
C/Species: Pseudomonas syringae pv. tomato
C/Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C/Accession: C41225
R/Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A/Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer
A/Reference number: A41225; M01D:92020961
A/Accession: C41225
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-5 <CHA>

Query Match
Best Local Similarity 36.4%; Score 20; DB 2; Length 5;
Matches 4; Conservative 0; Pred. No. 2.8e+05; Mismatches 1; Indels 0; Gaps 0;
DB 1 HPKIV 5

RESULT 2
PT0080
60K Ca binding protein - edible frog (fragment)
C/Species: Rana esculenta (edible frog)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PT0080
R/Trevoso, S.; Zorzet, F.; Chiozzi, P.; Melandri, P.; Volpe, P.; Pozzan, T.
Biochem. Biophys. Res. Commun. 175, 444-450, 1991
A/Title: Frog brain expresses a 60 kDa Ca2+ binding protein similar to mammalian calr
A/Reference number: PT0080; M01D:91207333
A/Accession: PT0080
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <TRE>

Query Match
Best Local Similarity 36.4%; Score 20; DB 2; Length 9;
Matches 4; Conservative 0; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;
DB 3 LVFF 6

RESULT 3

Cytochrome-c oxidase (EC 1.9.3.1) chain VII b, cardiac - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Jul-1999
 C:Accession: S65387; S65386
 R:Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
 Eur. J. Biochem. 230, 235-241, 1995
 A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
 A:Reference number: S65372; MUID:95324529
 A:Accession: S65387
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <SCH>
 A:Accession: S65386
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <SC2>
 C:Keywords: cardiac muscle; heart; oxidoreductase

Query Match

Best Local Similarity 32.7%; Score 18; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOK 4
 |||
 DB 2 HOK 4

RESULT 4

Fc epsilon RIIB - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
 C:Accession: A46474
 R:Richards, M.L.; Katz, D.H.; Liu, F.T.
 J. Immunol. 147, 1067-1074, 1991
 A:Title: Complete genomic sequence of the murine low affinity Fc receptor for IgE. Demor
 A:Reference number: A46474; MUID:91318149
 A:Accession: A46474
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-6 <RIC>
 A:Experimental source: BALB C, splenic B cells
 A>Note: sequence extracted from NCBI backbone (NCBIP:45428)

Query Match 29.1%; Score 16; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HH 2
 |||
 DB 4 HH 5

RESULT 5

phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize
 C:Species: Zea mays (maize)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
 C:Accession: S13889
 R:Jiao, J.; Chollet, R.
 Arch. Biochem. Biophys. 283, 300-305, 1990
 A:Title: Regulatory phosphorylation of serine-15 in maize phosphoenolpyruvate carboxylase
 A:Reference number: S13889; MUID:91112741
 A:Accession: S13889
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <TIA>
 C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match

29.1%; Score 16; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HH 2
 |||
 DB 1 HH 2

RESULT 6

glucuronokinase (EC 2.7.1.12), thermoresistant - Escherichia coli (fragment)
 C:Species: Escherichia coli
 C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999
 C:Accession: S74176
 R:izu, R.; Adachi, O.; Yamada, M.
 FEBS Lett. 394, 14-16, 1996
 A:Title: Purification and characterization of the Escherichia coli thermoresistant gl
 A:Reference number: S74176; MUID:97074194
 A:Accession: S74176
 A:Molecule type: protein
 A:Residues: 1-10 <IZU>
 A:Experimental source: strain K-12
 C:Genetics:
 A:Gene: gntK
 C:Keywords: dimer; phosphotransferase

Query Match 29.1%; Score 16; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HH 2
 |||
 DB 7 HH 8

RESULT 7

cellulase (EC 3.2.1.4) - Clostridium thermocellum (fragment)
 N:Alternate names: endo-1,4-beta-glucanase
 C:Species: Clostridium thermocellum
 C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 22-Nov-1996
 C:Accession: S21273
 R:Romaniec, M.P.M.; Fauth, U.; Kobayashi, T.; Huskisson, N.S.; Barker, P.J.; Demain,
 Biochem. J. 283, 69-73, 1992
 A:Title: Purification and characterization of a new endoglucanase from Clostridium th
 A:Reference number: S21273; MUID:92231850
 A:Accession: S21273
 A:Molecule type: protein
 A:Residues: 1-8 <ROM>
 C:Function:
 A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as
 A:Pathway: cellulose degradation
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 27.3%; Score 15; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 FAE 10
 |||
 DB 4 FAE 6

RESULT 8

parathyroid hormone-like protein, humoral hypercalcemia of malignancy - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
 C:Accession: A61102
 R:Meir, E.C.; Butts, W.J.; Morris, C.A.; Brady, T.G.; Insogna, K.L.
 Endocrinology 123, 2744-2751, 1988
 A:Title: Isolation of 16,000-Dalton parathyroid hormone-like proteins from two animal
 A:Reference number: A61102; MUID:89064600

A:Accession: A61102
 A:Molecule type: protein
 A:Residues: 1-9 <MEI>
 A:Experimental source: apocrine cell adenocarcinoma
 C:Superfamily: parathyroid hormone-related protein; parathyroid hormone homology
 C:Keywords: hormone; humoral hypercalcemia

Query Match 27.3%; Score 15; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 HQKL 5
 DB 6 HQL 9

RESULT 9
 T31612
 hypothetical protein Y50E8A.h - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T31612
 R:Steward, C.
 submitted to the EMBL Data Library, September 1999
 A:Reference number: Z21047
 A:Accession: T31612
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-9 <WIL>
 A:Cross-references: EMBL:AL117200; NID:e1549770; PIDN:CB55051.1; CESP:Y50E8A.h
 A:Experimental source: clone Y50E8A
 C:Genetics:
 A:Gene: CESP:Y50E8A.h

Query Match 27.3%; Score 15; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HHOK 4
 DB 5 HREK 8

RESULT 10
 S10920
 venom protein HR-3 - oriental hornet (fragment)
 C:Species: Vespa orientalis (oriental hornet)
 C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 08-Dec-1995
 C:Accession: S10920
 R:Tuchilbayev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
 Biochemistry (N.Y.) 53, 183-190, 1988
 A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. S
 A:Reference number: S06445
 A:Accession: S10920
 A:Molecule type: protein
 A:Residues: 1-9 <TUI>
 C:Keywords: venom

Query Match 27.3%; Score 15; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 HOKLV 6
 DB 4 HEFLV 8

RESULT 11
 B39504
 octamer-binding protein, Ku-like, 83K chain - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 30-Sep-1993
 C:Accession: B39504

R;May, G.; Sutton, C.; Gould, H.
 J. Biol. Chem. 266, 3052-3059, 1991
 A:Title: Purification and characterization of Ku-2, an octamer-binding protein relate
 A:Reference number: A39504; MUID:91131605
 A:Accession: B39504
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <MAV>

Query Match 27.3%; Score 15; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 5 IVEFAE 10
 DB 1 MVEPME 6

RESULT 12
 PT0310
 Ig heavy chain CRD3 region (clone 6-97) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0310
 R;Tamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
 A:Reference number: PT0222; MUID:91108337
 A:Accession: PT0310
 A:Molecule type: DNA
 A:Residues: 1-10 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 27.3%; Score 15; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 6.8e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LVFF 8
 DB 3 LVWF 6

RESULT 13
 PH0807
 T-cell receptor alpha chain (J4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PH0807
 R;Caanovna, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A:Title: T cell receptor genes in a series of class I major histocompatibility comple
 allelic exclusion and antigen-specific repertoire.
 A:Reference number: PH0746; MUID:92078846
 A:Accession: PH0807
 A:Molecule type: mRNA
 A:Residues: 1-10 <CAS>
 A:Cross-references: EMBL:X60916
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 27.3%; Score 15; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6.8e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 VFF 8
 DB 7 IFF 9

RESULT 14
 A30812
 sex pheromone CCF10 - Enterococcus faecalis

C:Species: Enterococcus faecalis
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
 C:Accession: A30812
 R:Morit, M.; Sakagami, Y.; Ishii, Y.; Ito, A.; Kitada, C.; Fujino, M.; Adait, J.C.; Du
 J. Biol. Chem. 263, 14574-14578, 1988
 A:Title: Structure of CCF10, a peptide sex pheromone which induces conjugative transfer
 A:Reference number: A30812; MUID:89008313
 A:Accession: A30812
 A:Molecule type: protein
 A:Residues: 1-7 <MOR>

Query Match 25.5%; Score 14; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 KLV 7
 DB 4 KLV 6

RESULT 15

B20569
 serum amyloid P-component - smooth dogfish (fragment)
 C:Species: Mustelus canis (smooth dogfish)
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Jun-1993
 C:Accession: B20569; A05074
 R:Robey, F.A.; Tanaka, T.; Liu, T.Y.
 J. Biol. Chem. 258, 3889-3894, 1983
 A:Title: Isolation and characterization of two major serum proteins from the dogfish, M.
 A:Reference number: A92419; MUID:83160932
 A:Accession: B20569
 A:Molecule type: protein
 A:Residues: 1-9 <ROB>
 C:Keywords: amyloid

Query Match 25.5%; Score 14; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 OKLV 7
 DB 5 KSLIF 9

RESULT 16

PH0113
 alpha-amylase (EC 3.2.1.1) III - rice (fragment)
 C:Species: Oryza sativa (rice)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 07-May-1999
 C:Accession: PH0113
 R:Chiba, Y.; Niede, Y.; Nakajima, T.; Ichishima, E.
 Agric. Biol. Chem. 55, 901-902, 1991
 A:Title: Unique enzymatic properties of alpha-amylase-III from suspension-cultured rice
 A:Reference number: PH0113; MUID:91234351
 A:Accession: PH0113
 A:Molecule type: protein
 A:Residues: 1-10 <CHR>
 A:Experimental source: cv. Sasanishiki
 C:Function:
 A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A:Pathway: glycogen/starch degradation
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 25.5%; Score 14; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OKLV 6
 DB 6 OKLV 9

RESULT 17

S43631
 cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, cardiac - rainbow trout (fragment)
 C:Species: Oncorhynchus mykiss (rainbow trout)
 C:Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
 C:Accession: S43631
 R:Freund, R.; Kadenbach, B.
 Eur. J. Biochem. 221, 1111-1116, 1994
 A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cyto
 A:Reference number: S43624; MUID:94237150
 A:Accession: S43631
 A:Molecule type: protein
 A:Residues: 1-10 <FRE>
 A:Note: The source is designated as Salmo gairdneri
 C:Genetics:
 A:Genome: nuclear
 C:Keywords: cardiac muscle; heart; membrane-associated complex; mitochondrion; oxidor

Query Match 25.5%; Score 14; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 OKL 5
 DB 8 OKL 10

RESULT 18

T46627
 hypothetical protein c4 - loblolly pine
 C:Species: Pinus taeda (loblolly pine)
 C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
 C:Accession: T46627
 R:Chang, S.; Purves, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
 submitted to the EMBL Data Library, July 1995
 A:Description: Cloning of a chitinase homolog which lacks chitin binding sites and is
 A:Reference number: Z23105
 A:Accession: T46627
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-4 <CHA>
 A:Cross-references: EMBL:U01309; NID:9974285; PID:9974292
 A:Experimental source: Strain 56PTX56PT3; 8 month seedlings

Query Match 23.6%; Score 13; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLV 6
 DB 2 KLV 4

RESULT 19

S71349
 beta-crystallin B2 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 07-May-1999
 C:Accession: S71349
 R:Dirks, R.P.H.; Kraft, H.J.; van Genesen, S.T.; Klok, E.J.; Pfundt, R.; Schoenmakers
 Eur. J. Biochem. 239, 23-32, 1996
 A:Title: The cooperation between two silencers creates an enhancer element that contr
 A:Reference number: S71349; MUID:96305362
 A:Accession: S71349
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-6 <DIR>
 A:Cross-references: EMBL:X83671
 A:Experimental source: strain Wistar; lens epithelial cells
 C:Genetics:
 A:Gene: CRYBB2

Query Match 23.6%; Score 13; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HQ 3
 1 1
 Db 5 HQ 6

RESULT 20

PT0368
 Ig gamma chain C region (gamma-1) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-1996
 C:Accession: PT0368
 R:Millili, M.; Fougereau, M.; Guglielmi, P.; Schliff, C.
 M:Immunol. 28: 753-761, 1991
 A:Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.
 A:Reference number: PT0368; MUID:91312348
 A:Accession: PT0368
 A:Molecule type: mRNA
 A:Residues: 1-8 <MIL>
 A:Experimental source: fetal liver
 C:Keywords: immunoglobulin

Query Match 23.6%; Score 13; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HQ 3
 1 1
 Db 2 HQ 3

RESULT 21

S55696
 phosphoenolpyruvate carboxykinase - Trypanosoma brucei
 C:Species: Trypanosoma brucei
 C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
 C:Accession: S55696
 R:Hunt, M.; Koehler, P.
 Biochim. Biophys. Acta 1249, 15-22, 1995
 A:Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Try
 A:Reference number: S55696; MUID:95284106
 A:Accession: S55696
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <HUN>

Query Match 23.6%; Score 13; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 HQ 5
 1 1
 Db 5 HKNL 8

RESULT 22

S65388
 cytochrome-c oxidase (EC 1.9.3.1) chain VII c, hepatic - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
 C:Accession: S65388; S65389
 R:Schaeffer, H.; Noack, H.; Halang, W.; Brandt, U.; von Jagow, G.
 Eur. J. Biochem. 230, 235-241, 1995
 A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
 A:Reference number: S65372; MUID:95324529
 A:Accession: S65388
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <SCH>
 A:Accession: S65389
 A:Status: preliminary
 A:Molecule type: protein

A:Residues: 1-10 <SC2>
 C:Superfamily: cytochrome-c oxidase chain VIIc
 C:Keywords: oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
 Best Local Similarity 25.0%; Pred. No. 1.7e+04;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HKOK 4
 1 1
 Db 2 HYE 5

RESULT 23

S30348
 clotting protein - signal crayfish
 C:Species: Pacifastacus leniusculus (signal crayfish)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S30348
 R:Kopacek, P.; Hall, M.; Soederhagell, K.
 Eur. J. Biochem. 213, 591-597, 1993
 A:Title: Characterization of a clotting protein, isolated from plasma of the freshwater
 A:Reference number: S30348; MUID:93238739
 A:Accession: S30348
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <KOP>

Query Match 23.6%; Score 13; DB 2; Length 10;
 Best Local Similarity 33.3%; Pred. No. 1.7e+04;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 HOKLVF 7
 1 1
 Db 2 HSNLEY 7

RESULT 24

S43625
 cytochrome-c oxidase (EC 1.9.3.1) chain Va, hepatic - rainbow trout (fragment)
 C:Species: Oncorhynchus mykiss (rainbow trout)
 C>Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
 C:Accession: S43625
 R:Freund, R.; Kadenbach, B.
 Eur. J. Biochem. 221, 1111-1116, 1994
 A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cyto
 A:Reference number: S43624; MUID:94237150
 A:Accession: S43625
 A:Molecule type: protein
 A:Residues: 1-10 <FRE>
 A:Note: the source is designated as Salmo gairdneri
 C:Genetics:
 A:Genome: nuclear
 C:Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.7e+04;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HOKL 5
 1 1
 Db 2 HAKV 5

RESULT 25

PT0284
 Ig heavy chain CRD3 region (clone 4-97) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0284
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an

A:Reference number: PT0222; MUID:91108337
A:Accession: PT0284
A:Molecule type: DNA
A:Residues: 1-10 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; Immunoglobulin

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 OKLVFF 8
|||
Db 3 OQLANF 8

RESULT 26
B45482
Platelet activating factor acetylhydrolase - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 05-May-1995
C:Accession: B45482
R:Stafforini, D.M.; Rollins, E.N.; Prescott, S.M.; McIntyre, T.M.
J. Biol. Chem. 268, 3857-3865, 1993
A:Title: The platelet-activating factor acetylhydrolase from human erythrocytes. Purified
A:Reference number: A45482; MUID:93179380
A:Accession: B45482
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <STK>

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 LVVF 8
|||
Db 3 LVVF 6

RESULT 27
T13838
cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipes biporus mitochondrion (fragment)
C:Species: mitochondrion Bipes biporus
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: T13838
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A:Title: Two novel gene orders and the role of light-strand replication in rearrangement
A:Reference number: Z17789; MUID:97153826
A:Accession: T13838
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <MAC>
A:Cross-references: EMBL:U71335; NID:q1753232; PID:q1753235; PIDN:AA848271.1
C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FFA 9
|||
Db 7 FFS 9

RESULT 28
T13976
cytochrome-c oxidase (EC 1.9.3.1) chain I - Chemidophorus tigris mitochondrion (fragment)
C:Species: mitochondrion Chemidophorus tigris

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: T13976
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A:Title: Two novel gene orders and the role of light-strand replication in rearrangement
A:Reference number: Z17789; MUID:97153826
A:Accession: T13976
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <MAC>
A:Cross-references: EMBL:U71332; NID:q1753236; PID:q1753239; PIDN:AA848274.1
C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FFA 9
|||
Db 7 FFS 9

RESULT 29
T17057
cytochrome-c oxidase (EC 1.9.3.1) chain I - Crotaphytus collaris mitochondrion (frag
C:Species: mitochondrion Crotaphytus collaris
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C:Accession: T17057
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A:Title: Evolutionary shifts in three major structural features of the mitochondrial
A:Reference number: Z18674; MUID:97315309
A:Accession: T17057
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <MAC>
A:Cross-references: EMBL:U82681; NID:q3603108; PID:q3603111; PIDN:AA62272.1
C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FFA 9
|||
Db 7 FFS 9

RESULT 30
T12303
cytochrome-c oxidase (EC 1.9.3.1) chain I - Diposaurus dorsalis mitochondrion (frag
C:Species: mitochondrion Diposaurus dorsalis
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999
C:Accession: T12303
R:Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A:Title: Molecular tests of phylogenetic taxonomies: A general procedure and example
A:Reference number: Z17488; MUID:99162288
A:Accession: T12303
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <SCH>
A:Cross-references: EMBL:AF049857; NID:q4105726; PID:q4105729; PIDN:AA02514.1
C:Genetics:
A:Genome: mitochondrion
A:Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
Db 7 FFS 9

RESULT 31

T14019

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Eremias grammica mitochondrion (fragment)

C:Species: mitochondrion Eremias grammica

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

C:Accession: T14019

R:Macay, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.

Mol. Biol. Evol. 14, 91-104, 1997

A:Title: Two novel gene orders and the role of light-strand replication in rearrangement

A:Reference number: 217789; MUID:97153826

A:Accession: T14019

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <MAC>

A:Cross-references: EMBL:U71331; NID:91753240; PID:91753243; PIDN:AAB48277.1

C:Genetics:

A:Genome: mitochondrion

A:Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
Db 7 FFS 9

RESULT 32

T17060

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Gambelia wislizenii mitochondrion (fragment)

C:Species: mitochondrion Gambelia wislizenii

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999

C:Accession: T17060

R:Macay, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997

A:Title: Evolutionary shifts in three major structural features of the mitochondrial ge

A:Reference number: 218674; MUID:97315309

A:Accession: T17060

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <MAC>

A:Cross-references: EMBL:U82682; NID:93603120; PID:93603123; PIDN:AAC62281.1

C:Genetics:

A:Genome: mitochondrion

A:Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
Db 7 FFS 9

RESULT 33

T14043

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Liailis jicari mitochondrion (fragment)

C:Species: mitochondrion Liailis jicari

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

C:Accession: T14043

R:Macay, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.

Mol. Biol. Evol. 14, 91-104, 1997

A:Title: Two novel gene orders and the role of light-strand replication in rearrangem

A:Reference number: 217789; MUID:97153826

A:Accession: T14043

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <MAC>

A:Cross-references: EMBL:U71327; NID:91753244; PID:91753247; PIDN:AAB48280.1

C:Genetics:

A:Genome: mitochondrion

A:Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
Db 7 FFS 9

RESULT 34

T14054

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Mabuya aurata mitochondrion (fragment)

C:Species: mitochondrion Mabuya aurata

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

C:Accession: T14054

R:Macay, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.

Mol. Biol. Evol. 14, 91-104, 1997

A:Title: Two novel gene orders and the role of light-strand replication in rearrangem

A:Reference number: 217789; MUID:97153826

A:Accession: T14054

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <MAC>

A:Cross-references: EMBL:U71330; NID:91753248; PID:91753251; PIDN:AAB48283.1

C:Genetics:

A:Genome: mitochondrion

A:Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
Db 7 FFS 9

RESULT 35

T17066

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Oplurus cuvieri mitochondrion (fragment)

C:Species: mitochondrion Oplurus cuvieri

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999

C:Accession: T17066

R:Macay, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997

A:Title: Evolutionary shifts in three major structural features of the mitochondrial

A:Reference number: 218674; MUID:97315309

A:Accession: T17066

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <MAC>

A:Cross-references: EMBL:U82685; NID:93603136; PID:93603139; PIDN:AAC62293.1

C:Genetics:

A:Genome: mitochondrion

A:Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
DB 7 FFS 9

RESULT 36

T17069

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Phrynosoma douglasii mitochondrion (fragment)

C:Species: mitochondrion Phrynosoma douglasii

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999

C:Accession: T17069

R:Maccey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997

A:Title: Evolutionary shifts in three major structural features of the mitochondrial gene

A:Reference number: Z18674; MUID:97315309

A:Accession: T17069

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <SCH>

A:Cross-references: EMBL:U82686; NID:g3603144; PID:g3603147; PIDN:AAC62299.1

C:Genetics:

A:Genome: mitochondrion

A>Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match

23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
DB 7 FFS 9

RESULT 37

T12308

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Sator angustus mitochondrion (fragment)

C:Species: mitochondrion Sator angustus

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999

C:Accession: T12308

R:Schulte, J.A.; Maccey, J.R.; Larson, A.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 367-376, 1998

A:Title: Molecular tests of phylogenetic taxonomies: A general procedure and example

A:Reference number: Z17488; MUID:99162288

A:Accession: T12308

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <SCH>

A:Cross-references: EMBL:AF049859; NID:g4105734; PID:g4105737; PIDN:AAD02520.1

C:Genetics:

A:Genome: mitochondrion

A>Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match

23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
DB 7 FFS 9

RESULT 38

T17072

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Sauromalus obesus mitochondrion (fragment)

C:Species: mitochondrion Sauromalus obesus

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999

C:Accession: T17072

OY 7 FFA 9
11:
DB 7 FFS 9

R:Maccey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997

A:Title: Evolutionary shifts in three major structural features of the mitochondrial

A:Reference number: Z18674; MUID:97315309

A:Accession: T17072

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <MAC>

A:Cross-references: EMBL:U82687; NID:g3603152; PID:g3603155; PIDN:AAC62305.1

C:Genetics:

A:Genome: mitochondrion

A>Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match

23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
DB 7 FFS 9

RESULT 39

T12312

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Sceloporus graciosus mitochondrion (fragm

C:Species: mitochondrion Sceloporus graciosus

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999

C:Accession: T12312

R:Schulte, J.A.; Maccey, J.R.; Larson, A.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 367-376, 1998

A:Title: Molecular tests of phylogenetic taxonomies: A general procedure and example

A:Reference number: Z17488; MUID:99162288

A:Accession: T12312

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <SCH>

A:Cross-references: EMBL:AF049860; NID:g4105738; PID:g4105741; PIDN:AAD02523.1

C:Genetics:

A:Genome: mitochondrion

A>Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match

23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
DB 7 FFS 9

RESULT 40

T12316

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Uma scoparia mitochondrion (fragment)

C:Species: mitochondrion Uma scoparia

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999

C:Accession: T12316

R:Schulte, J.A.; Maccey, J.R.; Larson, A.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 367-376, 1998

A:Title: Molecular tests of phylogenetic taxonomies: A general procedure and example

A:Reference number: Z17488; MUID:99162288

A:Accession: T12316

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-10 <SCH>

A:Cross-references: EMBL:AF049861; NID:g4105742; PID:g4105745; PIDN:AAD02526.1

C:Genetics:

A:Genome: mitochondrion

A>Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match

23.6%; Score 13; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 7 FFA 9
||:
Db 7 FFS 9

RESULT 41

T12321
cytochrome-c oxidase (EC 1.9.3.1) chain I - Uta stansburiana mitochondrion (fragment)
C:Species: mitochondrion Uta stansburiana
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999
C:Accession: T12321
R:Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.
Mol. Phylogenet. Evol. 10, 367-376, 1998
A:Title: Molecular tests of phylogenetic taxonomies: A general procedure and example us
A:Reference number: 217488; MUID:99162288
A:Accession: T12321
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <SCH>
A:Cross-references: EMBL:AF049863; NID:94105750; PID:94105753; PIDN:AAD02532.1
C:Genetics:
A:Genome: mitochondrion
A>Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
||:
Db 7 FFS 9

RESULT 42

T14219
cytochrome-c oxidase (EC 1.9.3.1) chain I - Xenosaurus grandis mitochondrion (fragment)
C:Species: mitochondrion Xenosaurus grandis
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T14219
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A:Title: Two novel gene orders and the role of light-strand replication in rearrangement
A:Reference number: Z17789; MUID:97153826
A:Accession: T14219
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <MAC>
A:Cross-references: EMBL:U71333; NID:95739536; PIDN:AAC62821.1; PID:91753275
C:Genetics:
A:Genome: mitochondrion
A>Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 23.6%; Score 13; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
||:
Db 7 FFS 9

RESULT 43

JQ1273
neuropeptide Antho-kamide - sea anemone (Anthopleura elegantissima)
C:Species: Anthopleura elegantissima
C>Date: 31-Mar-1992 #sequence_revision 04-Dec-1992 #text_change 08-Dec-1995
C:Accession: JQ1273
R:Notacker, H.P.; Rinehart, K.L.; Grimmelikhuijzen, C.J.P.

Biochem. Biophys. Res. Commun. 179, 1205-1211, 1991
A:Title: Isolation of L-3-phenylacetyl-Phe-Lys-Ala-NH₂ (Antho-kamide), a novel neuro
A:Reference number: JQ1273; MUID:92028852
A:Accession: JQ1273
A:Molecule type: protein
A:Residues: 1-4 <NOT>

C:Comment: The carboxyl-terminal amide probably arises from cleavage of a following 9
C:Keywords: amidated carboxyl end; neuropeptide; phenylacetylation
F:1/Modified site: L-3-phenylacetic acid (Phe) #status experimental
F:4/Modified site: amidated carboxyl end (Ala) #status experimental

Query Match 21.8%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FF 8
||:
Db 1 FF 2

RESULT 44

A32480
achatin-I - giant African snail
N:Contents: achatin-II
C:Species: Achatina fulica (giant African snail)
C>Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 17-Mar-1999
C:Accession: A32480
R:Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.;
Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989
A:Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica f
A:Reference number: A32480; MUID:89273351
A:Accession: A32480
A:Molecule type: protein
A:Residues: 1-4 <RAM>

A>Note: stereochemistry of the active form confirmed by chemical synthesis
R:Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nom
FEBS Lett. 307, 253-256, 1992
A:Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous ne
(H-Gly-Phe-Ala-Asp-OH).

A:Reference number: A44691; MUID:92354723
A:Contents: annotation; X-ray crystallography, 0.85 angstroms
A>Note: achatin-II has L-phenylalanine
C:Keywords: D-amino acid
F:2/Modified site: D-phenylalanine (Phe) #status experimental

Query Match 21.8%; Score 12; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 FAE 10
||:
Db 2 FAD 4

RESULT 45

A60986
N-formyl oligopeptide - Escherichia coli (fragment)
C:Species: Escherichia coli
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C:Accession: A60986
R:Broom, M.F.; Mellor, D.M.; Chadwick, V.S.
Experientia 45, 1097-1099, 1989
A:Title: Purification and amino acid sequencing of naturally occurring N-formyl-methi
A:Reference number: A60986; MUID:90092408
A:Accession: A60986
A:Molecule type: protein
A:Residues: 1-6 <BRO>

C:Comment: This hexapeptide was the longest of several N-formyl oligopeptides reporte
F:1/Modified site: N-formylmethionine #status experimental

Query Match 21.8%; Score 12; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 LVF 7
11
Db 1 MVF 3

RESULT 46

159142

Platelet-derived growth factor B chain - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C/Accession: 159142
R/Peptide: M.; Gazit, A.; Arnsperg, P.; Aronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 2693-2697, 1989
A/Title: Generation of fibrosarcomas in vivo by a retrovirus that expressed the normal F
A/Reference number: 159142; MUID:89202393
A/Accession: 159142
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-6 <RES>
A/Cross-references: GB:M26180; NID:g516624; PIDN:AAA39905.1; PID:g516625

Query Match 21.8%; Score 12; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 LVF 7
11
Db 1 MVF 3

RESULT 47

A43129

neuropeptide GnFRFamide - tapeworm (Moniezia expansa)
C/Species: Moniezia expansa
C/Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 14-Nov-1997
C/Accession: A43129
R/Molecule: A.; Shaw, C.; Halton, D.; Thim, L.
Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993
A/Title: GnFRFamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep t
A/Reference number: A43129; MUID:93312289
A/Accession: A43129
A/Molecule type: protein
A/Residues: 1-6 <MAU>
C/Keywords: amidated carboxyl end; neuropeptide
F/6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 21.8%; Score 12; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FF 8
11
Db 3 FF 4

RESULT 48

PT0246

Ig heavy chain CDR3 region (clone 2-103D) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0246
R/Yamada, M.; Maeser, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A/Reference number: PT0222; MUID:91108337
A/Accession: PT0246
A/Molecule type: DNA
A/Residues: 1-7 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 21.8%; Score 12; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 HOKL 5
11
Db 1 HEVL 4

RESULT 49

146868

alpha-myosin heavy chain - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C/Accession: 146868
R/Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A/Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventric
A/Reference number: 146868; MUID:84221901
A/Accession: 146868
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-7 <FRI>
A/Cross-references: GB:K01698; NID:g165538; PIDN:AAA31415.1; PID:g165539

Query Match 21.8%; Score 12; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OKL 5
11
Db 1 OKM 3

RESULT 50

T13818

cytochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)
C/Species: Mitochondrion Myxine glutinosa (Atlantic hagfish)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C/Accession: T13818
R/Delatorre, C.; Bartel, V.; Tiller, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A/Title: The main features of the craniate mitochondrial DNA between the ND1 and the
A/Reference number: Z17775; MUID:97398704
A/Accession: T13818
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-8
A/Cross-references: EMBL:Y09527; NID:g2340019; PIDN:CAA70718.1; PID:g2340022
C/Genetics:
A/Keywords: mitochondrion
A/Note: COI

Query Match 21.8%; Score 12; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FF 8
11
Db 7 FF 8

Search completed: October 29, 2002, 09:38:49
Job time : 15 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 09:31:37 ; Search time 11 Seconds

(without alignments)
35.200 Million cell updates/sec

Title: US-09-724-842a-27
Perfect score: 55
Sequence: 1 HHQKLVFAE 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 349

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: SWISSProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	32.7	10	1	COXM_RAT
2	16	29.1	5	1	RE11_LITRU
3	16	29.1	5	1	RE21_LITRU
4	16	29.1	10	1	PAP1_PARMA
5	15	27.3	5	1	UC22_MAZE
6	15	27.3	7	1	FR22_MSCU
7	15	27.3	10	1	RCA_PINPS
8	14	25.5	7	1	CCF1_ENTFA
9	14	25.5	8	1	CPD1_ENTFA
10	14	25.5	9	1	SAMP_MUSCA
11	14	25.5	10	1	COXK_ONCMY
12	13	23.6	8	1	UPRA_HUMAN
13	13	23.6	10	1	COXA_ONCMY
14	13	23.6	10	1	COXO_RAT
15	12	21.8	4	1	ACH1_ACHFU
16	12	21.8	5	1	FFKA_ANTEL
17	12	21.8	5	1	PAP2_PARMA
18	12	21.8	5	1	RE32_LITRU
19	12	21.8	6	1	FAFP_MONEX
20	12	21.8	5	1	FAFP_MONEX
21	12	21.8	8	1	B44K_PORGI
22	12	21.8	9	1	FIIB_ERYDA
23	12	21.8	10	1	COXO_THOBS
24	12	21.8	10	1	FAFP_MONEX
25	12	21.8	10	1	FAFP_MONEX
26	12	21.8	10	1	FIIB_CERST
27	12	21.8	10	1	MOSO_CLYXA
28	12	21.8	10	1	TKNK_PIG
29	12	21.8	10	1	TKU2_UREUN
30	12	21.8	10	1	TPIS_NICPL
31	12	21.8	10	1	TRP6_LEUMA
32	12	21.8	10	1	TRP7_LEUMA
33	11	20.0	7	1	CHOX_ALCSP

34	11	20.0	7	1	HT7_PIG	P01153 sus scrofa
35	11	20.0	7	1	UF03_MOUSE	P38641 mus musculus
36	11	20.0	8	1	AKR_TABAT	P14595 tabanus atr
37	11	20.0	8	1	HTF2_PERAM	P04549 periplaneta
38	11	20.0	9	1	FAR5_PANRE	P82661 panagrellina
39	11	20.0	9	1	ULAK_MOUSE	P99031 mus musculus
40	11	20.0	10	1	BPP2_BOTIN	P30422 botriops in
41	11	20.0	10	1	FAR6_PANRE	P82660 panagrellina
42	11	20.0	10	1	GON1_PETMA	P13385 petromyzon
43	11	20.0	10	1	HTF2_CARMO	P16353 heliothis z
44	11	20.0	10	1	HTF_HELZE	P14596 tabanus atr
45	11	20.0	10	1	Q20B_COMTE	P80465 comanonas t
46	11	20.0	10	1	Q20B_COMTE	P30425 botriops in
47	10	18.2	8	1	ACI_THUAL	P18691 thunnus alb
48	10	18.2	8	1	ALU1_CYPDO	P82152 cydia pomon
49	10	18.2	8	1	ALU1_CYPDO	P82152 cydia pomon
50	10	18.2	8	1	LCK8_LEUMA	P19990 leucophaea

ALIGNMENTS

RESULT 1	COXM_RAT	STANDARD;	PRT;	10 AA.
ID	P80431;			
AC	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DR	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)			
GN	COX/B.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN-WISTAR; TISSUE-Liver;			
RX	MEDLINE-95324529; PubMed-7601105;			
RA	Schaeffer H., Noack H., Halaangk W., Brandt U., von Jagow G.;			
RT	"Cytochrome-c oxidase in developing rat heart. Enzyme properties and			
RT	amino-terminal sequences suggest identity of the fetal heart and the			
RT	adult liver isoform."			
RL	Eur. J. Biochem. 230:235-241(1995).			
CC	-1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE			
CC	CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN			
CC	MITOCHONDRIAL ELECTRON TRANSPORT.			
CC	-1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) -> 4 ferricytochrome			
CC	c + 2 H(2)O.			
KW	Oxidoreductase; Mitochondrion.			
FT	NON_TER			
FT	SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;			
SO	SEQUENCE			
Query Match	32.7%;	Score 18;	DB 1;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 7.3e+02;		
Matches	3;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
DB	2 HOK 4			
DB	2 HOK 4			
RESULT 2	RE11_LITRU	STANDARD;	PRT;	5 AA.
ID	P82070;			
AC	01-MAR-2002 (Rel. 41, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DR	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Rubellididn 1.1.			
OS	Litoria rubella (Desert tree frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

```

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
  Tyler M.O., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
  'Litoria rubella', the skin peptide profile as a probe for the study
  of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
  ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MM=598; METHOD-FAB.
KM Amphibian skin.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match          29.1%; Score 16; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
   |||
DB 3 FFA 5

RESULT 3
RE21_LITRU          STANDARD;          PRT;          5 AA.
ID RE21_LITRU
AC P82071;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Rubellidin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
  Tyler M.O., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
  'Litoria rubella', the skin peptide profile as a probe for the study
  of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
  ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -1- MASS SPECTROMETRY: MM=626; METHOD-FAB.
KM Amphibian skin.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match          29.1%; Score 16; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
   |||
DB 3 FFA 5

RESULT 4
PAP1_PARMA          STANDARD;          PRT;          10 AA.
ID PAP1_PARMA
AC P81863;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE Pardaxin I (PXI) (Fragment).
OS Pardaxinus marmoratus (Red sea moose sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleidae; Soleidae; Pardaxinus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE-Skin secretion;
RA MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
  polypeptides from the secretion of the Red sea moose sole (Pardaxinus
  marmoratus)";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -1- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
  PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS IN
  MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS. SHOWN
  TO BE 5-10 TIMES MORE TOXIC, CYTOLYTIC AND ACTIVE IN MEMBRANE PORE
  FORMATION THAN PARDAXIN II.
CC -1- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A Tetramer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KM Toxin.
FT NON_TER
SQ SEQUENCE 10 AA; 1063 MW; D399C36760572DD9 CRC64;

Query Match          29.1%; Score 16; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
   |||
DB 2 FFA 4

RESULT 5
UC22_MAIZE          STANDARD;          PRT;          5 AA.
ID UC22_MAIZE
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE-Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
  Renollat J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
  genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
  PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.
DR MaizeDB; 123954; -.
FT NON_TER
SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

Query Match          27.3%; Score 15; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 VFF 8
   |||

```


Db 1 IFF 3

RESULT 6

FAR2_ASCSU STANDARD; PRT; 7 AA.

AC P31890;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DE 01-FEB-1996 (Rel. 33, Last annotation update)

OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and

OS Panagrellus redivivus.

OS Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;

OC Ascarididae; Ascaris.

OC NCBI_TaxId=6253; 6233;

RN [1]

RP SEQUENCE.

RC SPECIES-A.suum;

RX MEDLINE=93324431; PubMed=8332542;

RA Cowden C., Stretton A.O.W.;

RT "AF2, an Ascaris neurotrophin: Isolation, sequence, and bioactivity.";

RL Peptides 14:423-430(1993).

RN [2]

RP SEQUENCE.

RC SPECIES-P.redivivus;

RX MEDLINE=95060998; PubMed=7970891;

RA Maule A.G., Shaw C., Bowman J.W.;

RT "The FMRamide-like neuropeptide AF2 (Ascaris suum) is present in the

free-living nematode, Panagrellus redivivus (Nematoda, Rhabditidae).";

RL Parasitology 109:351-356(1994).

CC -1- FUNCTION: HAS EFFECTS ON MUSCLE TENSION.

CC -1- TISSUE SPECIFICITY: FOUND IN THE NERVE REGIONS.

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)

CC FAMILY.

CC Neuropeptide; Amidation.

KW MOD.RES

FT SEQUENCE

SQ SEQUENCE 7 AA; 992 MW; 69DA073B5B1E350 CRC64;

Db 2 HOKLIF 7

Db 2 HEYLRP 7

Db 2 HEYLRP 7

Db 2 HEYLRP 7

Db 2 HEYLRP 7

Db 2 HEYLRP 7

Db 2 HEYLRP 7

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Db 2 HEYLRP 7

RA Costa P., Pionneau C., Bauw G., Dubos C., Bahman N., Kremer A.,

RT "Separation and characterization of needle and xylem maritime pine

RT proteins.";

RL Electrophoresis 20:1098-1108(1999).

CC -1- FUNCTION: ACTIVATION OF RUBISCO (RUBULOSE-1,5-BISPHOSPHATE

CARBOXYLATION OF THE EPISILON-AMINO GROUP OF LYSINE LEADING TO A

CC CARBOXYLATION OF THE EPISILON-AMINO GROUP OF LYSINE LEADING TO A

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CC CARBOXYLATION OF THE EPISILON-AMINO GROUP OF LYSINE LEADING TO A

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CC CARBOXYLATION OF THE EPISILON-AMINO GROUP OF LYSINE LEADING TO A

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OX NCBI_TaxID=1351;
RN [1]
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sakakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, CPD1.";
RL Science 226:849-850(1984).
CC -1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOLICIN PLASMID PPd1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match
Best Local Similarity 25.5%; Score 14; DB 1; Length 8;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 LVFF 8
DB 2 LVWF 5

RESULT 10
SAMP_MUSCA STANDARD; PRT; 9 AA.
AC P19095;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serum amyloid P-component (SAP) (Fragment).
OS Musculus canis (Smooth dogfish).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=7812;
RN [1]
RX MEDLINE=83160932; PubMed=6403520;
RA Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
RT dogfish, Mustelus canis, C-reactive protein and amyloid P
RT component.";
RL J. Biol. Chem. 258:3889-3894(1983).
CC -1- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -1- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -1- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.
DR InterPro: IPR001759; Pentaxin.
DR PROSITE: PS00289; PENTAXIN; PARTIAL.
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT DOMAIN 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match
Best Local Similarity 25.5%; Score 14; DB 1; Length 9;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 OKLVF 7
DB 5 KSLIF 9

RESULT 11
SAMP_ONCMY STANDARD; PRT; 10 AA.
AC P80332;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIa-heart (EC 1.9.3.1) (Fragment).

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OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadembach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR PIR: S43631; S43631.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1174 MW; 4CB81CAF772C3 CRC64;

Query Match
Best Local Similarity 25.5%; Score 14; DB 1; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 OKL 5
DB 8 OKL 10

RESULT 12
SAMP_HUMAN STANDARD; PRT; 8 AA.
ID UPAA_HUMAN
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Pasquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7, ITS MW IS: 12 kDa.
DR SWISS-2DPAGE: P30096; HUMAN.
FT VARIAT 1
FT NON_TER 5
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match
Best Local Similarity 23.6%; Score 13; DB 1; Length 8;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 LVFF 8
DB 3 LVWF 6

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RESULT 13
COXA_ONCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide VA (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proteoanchopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCB1_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and Viba
of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) -> 4 ferricytochrome
c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR PIR; S43625; S43625.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 10
SQ SEQUENCE 10 AA; 114 MW; C535C5B1AB02C3D CRC64;
Query Match 23.6%; Score 13; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 7e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 HOKL 5
DB 2 HARV 5
RESULT 14
COXA_RAT STANDARD; PRT; 10 AA.
AC P80432;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC, mitochondrial (EC 1.9.3.1)
(VIIC) (Fragment).
GN COX7C OR COX7CI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Liver, and Heart;
RX MEDLINE=95324529; PubMed=7601105;
RA Schlegel H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome c oxidase in developing rat heart. Enzymic properties and
amino-terminal sequences suggest identity of the fetal heart and the
adult liver isoform.";
RL Eur. J. Biochem. 230:235-241(1995).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) -> 4 ferricytochrome
c + 2 H(2)O.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;

Query Match 23.6%; Score 13; DB 1; Length 10;
Best Local Similarity 25.0%; Pred. No. 7e+03;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 HOKL 4
DB 2 HYEE 5
RESULT 15
ACH1_ACHFU STANDARD; PRT; 4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Achatin-I.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCB1_TaxID=6530;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC STRAIN=FERUSSAC; TISSUE=Ganglion;
RX MEDLINE=89273551; PubMed=2597281;
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA Novales E.T., Kanapl C.G., Takeuchi H., Nomoto K.;
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
fulica Ferussac containing a D-amino acid residue.";
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RP CHARACTERIZATION.
RC STRAIN=FERUSSAC; TISSUE=Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT "Purification of achatin-I from the atria of the African giant snail,
Achatina fulica, and its possible function.";
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=93014529; PubMed=1399265;
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA Iwashita T., Nomoto K.;
RT "Crystal structure and molecular conformation of achatin-I
(H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
D-amino acid residue.";
RL Int. J. Pept. Protein Res. 39:258-264(1992).
CC -1- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
DR PIR; A32480; A32480.
KW Hormone; D-amino acid.
FT MOD_RES 2
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;
Query Match 21.8%; Score 12; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 8 FAE 10
DB 2 FAD 4
RESULT 16
FFKA_ANTNL STANDARD; PRT; 4 AA.
AC P58705;
DT 01-MAR-2002 (Rel. 41, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Antho-Kaamide.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
 OC Nyantheae; Actinidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]
 RP SEQUENCE.
 RX PubMed=1681803;
 RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
 RT "Isolation of L-3-phenylacetyl-Phe-Lys-Ala-NH₂ (Antho-Kaamide), a
 novel neuropeptide from sea anemones.";
 RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
 RN [2]
 RP FUNCTION.
 RX PubMed=8397415;
 RA McFarlane I.D., Hudson D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two
 inhibitory neuropeptides, Antho-Kaamide and Antho-Ramide.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
 CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
 groups. May be involved in the expansion phase of feeding
 behaviour in sea anemones.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Neuron-specific.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1
 FT MOD_RES 4 4
 FT MOD_RES 4 4
 SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 21.8%; Score 12; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FF 8
 DB 1 FF 2

RESULT 17
 PAP2_PAPMA STANDARD; PRT; 5 AA.
 ID PAP2_PAPMA
 AC P81864;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pardaxin II (PxiI) (Fragment).
 OS Pardachirus marmoratus (Red sea moose sole).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Soleiidae; Soleidae; Pardachirus.
 OX NCBI_TaxID=31087;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Skin secretion;
 RX MEDLINE=87057369; PubMed=3782138;
 RA Lazarovici P., Primor N., Loew L.M.;
 RT "Purification and pore-forming activity of two hydrophobic
 polypeptides from the secretion of the Red sea moose sole (Pardachirus
 marmoratus).";
 RL J. Biol. Chem. 261:16704-16713(1986).
 CC -1- FUNCTION: EXHIBITS UNSUAL SHARK REPELLENT AND SURFACTANT
 PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
 IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
 CC -1- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A Tetramer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PARAXIN FAMILY.
 KW Toxin.
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 21.8%; Score 12; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FF 8
 DB 2 FF 3

RESULT 18
 RE32_LITRU STANDARD; PRT; 5 AA.
 ID RE32_LITRU
 AC P82072;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 3.1.
 OS Litorea rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litorea.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 'Litorea rubella', the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=655; METHOD=FM.
 KW Amphibian skin; Amidation.
 FT MOD_RES 5 5
 FT MOD_RES 5 5
 SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 21.8%; Score 12; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FF 8
 DB 3 FF 4

RESULT 19
 RE32_LITRU STANDARD; PRT; 5 AA.
 ID RE32_LITRU
 AC P82073;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Rubellidin 3.2.
 OS Litorea rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litorea.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 'Litorea rubella'. Comparison with the skin peptides from Litorea
 rubella.";
 RL Aust. J. Chem. 52:0-0(1999).
 CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
 ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 KW Amphibian skin.

SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 21.8%; Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FF 8
11
DB 3 FF 4

RESULT 20

FARP_MONEX STANDARD; PRT; 6 AA.

AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
OS FMRamide-like neuropeptide GNFRRF-amide.
OC Moniezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellarian platyhelminths;
OC Rhabditiophora; Euteleostomi; Vertebrata; Medusozoa;
OC Neodermata; Cestoda; Eucestoda; Cyclophyllidae; Anoplocephalidae;
OC Moniezia.
OX NCBI_TaxID=28841;
RN [1]
RP SEQUENCE.

RA MEDLINE=93312289; PubMed=8323531;
MAule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFRamide: a novel FMRamide-immunoreactive peptide isolated from
the sheep tapeworm, Moniezia expansa."
RL Blochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC -1- FAMILY.

KW Neuropeptide; Amidation.
FT MOD.RES 6
SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match 21.8%; Score 12; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FF 8
11
DB 3 FF 4

RESULT 21

B44K_PORGI STANDARD; PRT; 8 AA.

AC P81866;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 44 kDa immunogenic protein (Fragment).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; CFB group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
OC Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE.

RA MEDLINE=20198497; PubMed=10731616;
Norriss J.M., Love D.N.;
RT "Serum antibody responses of cats to soluble whole cell antigens of
feline Porphyromonas gingivalis."
RL Vet. Microbiol. 73:37-48(2000).
CC -1- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
KM Antigen.
FT NON.TER 8
SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match 21.8%; Score 12; DB 1; Length 8;

Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOK 4
11
DB 3 YOK 5

RESULT 22

FIBB_ERYPA STANDARD; PRT; 9 AA.

AC P19346;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
OS Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.

RA MEDLINE=85289140; PubMed=3928610;
Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
patas monkey (Erythrocybus patas): their amino acid sequences,
restricted mutations, and a molecular phylogeny for macaques,
guenons, and baboons."
RL J. Biochem. 97:1487-1492(1985).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
AGGREGATION.

CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

DR PIR; D24180; D24180.
DR InterPro: IPR002181; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON.TER 1 9
SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 21.8%; Score 12; DB 1; Length 9;
Best Local Similarity 16.7%; Pred. No. 1e+05;
Matches 1; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 2 HOK 7
11
DB 1 NEVYLF 6

RESULT 23

COXO_THUOB STANDARD; PRT; 10 AA.

AC P80982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.

RC TISSUE-Heart, and Liver;
 RX MEDLINE-97454291; PubMed-9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 liver";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 c + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;

Query Match 21.8%; Score 12; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.1e+04;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 FAE 10
 :11
 Db 3 YAE 5

RESULT 24
 FARP_MANSE STANDARD; PRT; 10 AA.
 ID FARP_MANSE
 AC F18533;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRamide-like neuropeptide.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm). Insecta;
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Sphingidae; Sphingidae; Sphinginae; Manduca.
 OX NCBI_Taxid-7130;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-91045350; PubMed-2235684;
 RA Kinsan T.G., Teplow D.B., Phillips J.M., Riehm J.P., Rao K.R.,
 RA Hildebrand J.G., Homberg U., Kammer A.E., Jardine I., Griffin P.R.,
 RA Hunt D.F.;
 RT "A new peptide in the FMRamide family isolated from the CNS of the
 hawkmoth, Manduca sexta";
 RL Peptides 11:849-856(1990).
 CC -1- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN
 THE MAJOR POWER-PRODUCING FLIGHT MUSCLES, THE DORSAL LONGITUDINAL
 MUSCLES AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING
 FLIGHT BEHAVIOR PATTERNS.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC PIR: A43977; A43977.
 DR Amidation; Neuropeptide.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10
 FT SEQUENCE 10 AA; 1247 MW; D3C452295B1F2D2 CRC64;

Query Match 21.8%; Score 12; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 HOKLVE 7
 :11
 Db 5 HSFLEF 10

RESULT 25
 FARP_MATED STANDARD; PRT; 10 AA.
 ID FARP_MATED

AC P42560;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE FMRamide-like neuropeptide ALAGDHFFR-amide.
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_Taxid-6550;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-93047883; PubMed-1358534;
 RA Walker R.J.;
 RT "Neuroactive peptides with an Rfamide or Famide carboxyl terminal";
 RL Comp. Biochem. Physiol. 102C:213-222(1992).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 FT MOD_RES 10 10
 FT SEQUENCE 10 AA; 1180 MW; C2F80CC9C1EAA87D CRC64;

Query Match 21.8%; Score 12; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FF 8
 :11
 Db 7 FF 8

RESULT 26
 FIBB_CERSI STANDARD; PRT; 10 AA.
 ID FIBB_CERSI
 AC P14537;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 GN FGB.
 OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
 OX NCBI_Taxid-9807;
 RN [1]
 RP SEQUENCE.
 RA O'Neill P.B., Doolittle R.F.;
 RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences";
 RL Syst. Zool. 22:590-595(1973).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA). LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR InterPro: IPR002181; Fibrinogen.C.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
 KW Blood coagulation; Plasma.
 FT MOD_RES 1 1 FIBRINOPEPTIDE B.
 FT NON_TER 10 10
 FT SEQUENCE 10 AA; 1097 MW; 9402B2B2CDDDD33A CRC64;

Query Match 21.8%; Score 12; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HHOK 4
 :11
 Db 1 HDDK 4

RESULT 27
MOSO_CLYJA STANDARD; PRT; 10 AA.
AC P19962;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE [Gln-6]-mosact.
OS Clypeaster japonicus (Sand dollar).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Euechinozoa; Gnathostomata; Clypeasteroidea;
OC Clypeasteridae; Clypeaster.
OX NCBI_Taxid=7644;
RN [1]
RP SEQUENCE.
RC TISSUE-Egg jelly;
RA Suzuki N., Kurita M., Yoshino K., Kajima H., Nomura K., Yamaguchi M.;
RT Purification and structure of mosact and its derivatives from the
RT egg jelly of the sea urchin Clypeaster japonicus.";
RL Zool. Sci. 4:649-656(1987).
CC -1- FUNCTION: STIMULATES SPERM RESPIRATION AND MOTILITY.
SQ PIR, JN0025; JN0025.
SQ SEQUENCE 10 AA; 1019 MW; 9AFB032456DC5BA CRC64;

Query Match
Best Local Similarity 21.8%; Score 12; DB 1; Length 10;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 QKIV 6
1 1
1 1
DB 6 ONLI 9

RESULT 28
TKNK_PIG STANDARD; PRT; 10 AA.
AC P01292;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurokinin B (NKB) (Neuromedin K).
GN TAC3 OR NKMB.
OS Sus scrofa (Pig), and
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9823; 8406;
RN [1]
RP SEQUENCE.
RC SPECIES-Pig; TISSUE-Spinal cord;
RA MEDLINE=83282812; PubMed=6576785;
RA Kangawa K., Minamide N., Fukuda A., Matsuo H.;
RT "Neuromedin K: a novel mammalian tachykinin identified in porcine
RT spinal cord.";
RL Biochem. Biophys. Res. Commun. 114:533-540(1983).
RN [2]
RP SEQUENCE.
RC SPECIES-R. ridibunda; TISSUE-Brain;
RA MEDLINE=9204543; PubMed=1658233;
RA O'Harte F., Burcher E., Iovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin B: a novel NK1 tachykinin receptor agonist isolated with
RT neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
RN [1]
RP FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
RP EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
RP SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
RP MUSCLES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC PIR: A01560; SPRENK.
DR InterPro; IPRO02040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amlation.

FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1211 MW; E1FA7C62C9C9CA1 CRC64;

Query Match
Best Local Similarity 21.8%; Score 12; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FF 8
1 1
1 1
DB 5 FF 6

RESULT 29
TKU2_UREUN STANDARD; PRT; 10 AA.
AC P40752;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Urechis tinctorius.
OS Urechis tinctorius.
OC Eukaryota; Metazoa; Echinura; Xenopneusta; Urechidae; Urechis.
OX NCBI_Taxid=6432;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Ventral nerve cord;
RX MEDLINE=93236558; PubMed=8476410;
RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;
RT "Two novel tachykinin-related neuropeptides in the echinuroid worm,
RT Urechis tinctorius.";
RL Biochem. Biophys. Res. Commun. 192:1-6(1993).
CC -1- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL
CC MUSCLE OF THE ANIMAL.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amlation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 984 MW; 3F58DD79C9C87698 CRC64;

Query Match
Best Local Similarity 21.8%; Score 12; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 FF 8
1 1
1 1
DB 6 FF 7

RESULT 30
TPIS_NICPL STANDARD; PRT; 10 AA.
AC P19118;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).
OS Nicotiana glauca (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_Taxid=4092;
RN [1]
RP SEQUENCE.
RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;
RT "Alterations in the phenotype of plant cells studied by NH2-terminal
RT amino acid-sequence analysis of proteins electrophoretically
RT dimensional gel-separated total extracts.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate -> glyceralone
CC phosphate.
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC

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CC AND PLASTID.
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR PIR: A27617; A27617.
DR InterPro: IPR000652; Trioseph_isomerase.
DR Pfam: PF00121; TIM: 1.
DR PROSITE: PS00171; TIM: PARTIAL.
KM Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KM Pentose shunt.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1140 MW; 80B9D37862C9C9D1 CRC64;

Query Match
Best Local Similarity 21.8%; Score 12; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FF 8
DB 4 FF 5

RESULT 31
TRP6_LEUMA
ID TRP6_LEUMA STANDARD; PRT; 10 AA.
AC P81738;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Tachykinin-related peptide 6 (LemRP 6).
OS Leucophaea maderae (Madella cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Brain;
RX MEDLINE-97269266; PubMed-9114447;
RA Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT Madella cockroach: evidence for tissue-specific expression of
RT isoforms.";
RL Peptides 18:7-15(1997).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- MASS SPECTROMETRY: MW-1023.0; METHOD=MALDI.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KM Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1024 MW; C4469D79C9C87DD CRC64;

Query Match
Best Local Similarity 21.8%; Score 12; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FF 8
DB 6 FF 7

RESULT 32
TRP7_LEUMA
ID TRP7_LEUMA STANDARD; PRT; 10 AA.
AC P81739;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Tachykinin-related peptide 7 (LemRP 7).
OS Leucophaea maderae (Madella cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;

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RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Brain;
RX MEDLINE-97269266; PubMed-9114447;
RA Muren J.E., Naessel D.R.;
RT "Seven tachykinin-related peptides isolated from the brain of the
RT Madella cockroach: evidence for tissue-specific expression of
RT isoforms.";
RL Peptides 18:7-15(1997).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- MASS SPECTROMETRY: MW-1069.7; METHOD=MALDI.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KM Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1068 MW; C4541679C9C865BD CRC64;

Query Match
Best Local Similarity 21.8%; Score 12; DB 1; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 FF 8
DB 6 FF 7

RESULT 33
CHOX_ALCSP
ID CHOX_ALCSP STANDARD; PRT; 7 AA.
AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
OC Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE-8106769; PubMed-6997283;
RA Ohta-Fukuyama M., Miyake Y., Eml S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
RT oxidase from Alcaligenes sp.";
RL J. Biochem. 88:197-203(1980).
CC -1- CATALYTIC ACTIVITY: Choline + O(2) -> betaine aldehyde + H(2)O(2).
DR PIR: A15398; A15398.
KM Oxidoreductase.
FT MOD_RES 7
FT NON_TER 7
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match
Best Local Similarity 20.0%; Score 11; DB 1; Length 7;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 HHOK 4
DB 4 NHR 7

RESULT 34
HY7_PIG
ID HY7_PIG STANDARD; PRT; 7 AA.
AC P01153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Hypothalamic heptapeptide.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

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RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE-81213980; PubMed-62633778;
 RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
 RA Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
 RT "Isolation, structure and synthesis of a heptapeptide with in vitro
 RT ACHH-releasing activity from porcine hypothalamus.";
 RL Horm. Metab. Res. 13:228-232(1981).
 DR PIR: A01417; NYPG7
 SQ SEQUENCE 7 AA; 957 MW; 63264551F85059A0 CRC64;

Query Match 20.0%; Score 11; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 HXOK 4
 Db 4 HSYK 7

RESULT 35
 UF03_MOUSE
 ID UF03_MOUSE STANDARD; PRT; 7 AA.
 AC P36641;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE-95009907; PubMed-7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis";
 RL Electrophoresis 15:735-745(1994).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.1, ITS MW IS: 36 KDa.
 FT NON_TER
 SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DBD81B180 CRC64;

Query Match 20.0%; Score 11; DB 1; Length 7;
 Best Local Similarity 33.3%; Pred. No. 1e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 HOK 4
 Db 1 HEE 3

RESULT 36
 AKH_TABAT
 ID AKH_TABAT STANDARD; PRT; 8 AA.
 AC P14595;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Adipokine hormone (AKH) (Diptera corpora cardiaca factor I)
 DE (DCC I).
 OS Tabanus atratus (Horse fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha;
 CC Tabanidae; Tabanus.
 OX NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE-90046758; PubMed-2813385;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nechman R.J.;

RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -1- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTN / RPCH FAMILY.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 20.0%; Score 11; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 4 KLYE 7
 Db 1 QLT 4

RESULT 37
 HTP2_PERAM
 ID HTP2_PERAM STANDARD; PRT; 8 AA.
 AC P04549;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Hypertrehalosemic factor II (Neuropeptide H-II) (Periplaneta
 DE (Pex-CH-II) (Lep-CC-II) (Hypertrehalosemic neuropeptide II).
 OS Periplaneta americana (American cockroach).
 OS Blattella orientalis (Oriental cockroach), and
 OS Blattella orientalis (Oriental cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 CC Blattodea; Blattella; Periplaneta.
 OX NCBI_TaxID=6978; 7539; 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE-85046530; PubMed-6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L., Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry";
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE-84298179; PubMed-6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardiacacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE-90160053; PubMed-2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;

RX MEDLINE-90253659; PubMed-2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrichalosemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches *Leucophaea maderae*,
 RT *Gromphodromia portoricensis*, *Blattella germanica* and *Blattella orientalis*
 RT and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
 RT atom bombardment mass spectrometry";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: HYPERTRICHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH OF INSECTS.
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS.
 CC -1- SIMILARITY: BELONGS TO THE AKH / RHRH / RPCH FAMILY.
 DR PIR: A05170; A05170.
 DR PIR: S08996; S08996.
 DR PIR: B44960; B44960.
 DR PIR: B49823; B49823.
 DR Interfero; IP002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;
 Query Match 20.0%; Score 11; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 KLVF 7
 DB 1 QLVF 4

RESULT 38
 FAR6_PANRE STANDARD; PRT; 9 AA.
 ID FAR6_PANRE
 AC P82661;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRFamide-like neuropeptide PF5 (AMRNALVRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID-6233;
 RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffet C.L., Marks N.T., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of FMRFamide-related
 RT peptides (FARPs) from free-living nematode, *Panagrellus redivivus*,"
 RT Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -1- FUNCTION: MIOACTIVE.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 9 9 AMIDATION.
 FT MOD_RES 9 AA; 1077 MW; A0D112C72DD45406 CRC64;
 SQ SEQUENCE 9 AA; 1077 MW; A0D112C72DD45406 CRC64;
 Query Match 20.0%; Score 11; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 LVVF 8
 DB 6 LVVF 9

RESULT 39
 ULAK_MOUSE STANDARD; PRT; 9 AA.
 ID ULAK_MOUSE
 AC P89031;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 2D-0014LD)
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
 RA Cowthorne M.;
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 KDA.
 DR SWISS-2DPAGE; P99031; MOUSE.
 FT NON_TER 9 9
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 1106 MW; E1E842C3240B145A CRC64;
 Query Match 20.0%; Score 11; DB 1; Length 9;
 Best Local Similarity 16.7%; Pred. No. 1e+05;
 Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HHQV 6
 DB 3 NERKVI 8

RESULT 40
 BPP2_BOTIN STANDARD; PRT; 10 AA.
 ID BPP2_BOTIN
 AC P30423;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Bradykinin-potentiating peptide 54,3,1 (10C) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Quelana jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID-8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA MEDLINE-90351557; PubMed-2386615;
 RA Chtira A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from *Bothrops insularis* snake venom,"
 RT J. Protein Chem. 9:221-227(1990).
 CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
 CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
 CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 DR PIR: B37196; B37196.
 KW Hypotensive agent; Venom.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 AA; 1213 MW; 30C53546C761F773 CRC64;
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;
 Query Match 20.0%; Score 11; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.7e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HHQ 3
 DB 5 HPQ 7

RESULT 41
 FAR6_PANRE STANDARD; PRT; 10 AA.
 ID FAR6_PANRE
 AC P82660;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRamide-like neuropeptide PR6 (NGAFQFVRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of RMRamide-related
 RT peptides (FARPs) from free-living nematode, Panagrellus redivivus.";
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -1- FUNCTION: MYOACTIVE.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 10
 FT SEQUENCE 10 AA; 1132 MW; CB1E4C9D776C76D CRC64;

Query Match 20.0%; Score 11; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 OKLVEF 8
 DB 5 QPVRVF 10

RESULT 42
 GONI_PETMA STANDARD; PRT; 10 AA.
 AC P04378;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Gonadoliberin I (gonadotropin-releasing hormone I) (GNRH-I)
 DE (Luliberin I).
 OS Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 OX NCBI_TaxID=7757;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Brain;
 RX MEDLINE=86168192; PubMed=3514603;
 RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
 RT "Primary structure of gonadotropin-releasing hormone from lamprey
 RT brain.";
 RL J. Biol. Chem. 261:4812-4819(1986).
 CC -1- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND
 CC FOLLICLE-STIMULATING HORMONES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
 DR PIR: A01412; RHLMS.
 DR Interpro: IPR002012; GNRH.
 DR Pfam: PF00446; GNRH; 1.
 DR PROSITE: PS00473; GNRH; 1.
 KW Hormone; Amidation; Hypothalamus.
 FT MOD_RES 1 1
 FT MOD_RES 10 10
 FT SEQUENCE 10 AA; 1244 MW; IE4B36237B1735AB CRC64;

Query Match 20.0%; Score 11; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.7e+04;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 HOKL 5
 DB 2 HYSL 5

RESULT 43
 HTF2_CARMO STANDARD; PRT; 10 AA.
 AC P1385;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hypertrehalosemic factor II (HTF-II) (HRTII-II) (Hypertrehalosemic
 DE neuropeptide II).
 OS Carausius morosus (Indian stick insect), and
 OS Ectatosoma tiaratum (Stick insect).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Phasmatodea; Heteronemidae;
 OC Carausius.
 OX NCBI_TaxID=7022, 7024;
 RN [1]
 RP SEQUENCE.
 RC SPECIES-E. tiaratum; TISSUE-Corpus cardiaca;
 RX MEDLINE=87157103; PubMed=3828078;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structure of the hypertrehalosemic factor II from the
 RT corpus cardiaca of the Indian stick insect, Carausius morosus,
 RT determined by fast atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).
 RN [2]
 RN SEQUENCE.
 RP SPECIES-E. tiaratum; TISSUE-Corpus cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gryllodromia porteri, Blattella germanica and Blattella orientalis
 RT and of the stick insect Ectatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITE.
 RC SPECIES-C. morosus; TISSUE-Corpus cardiaca;
 RX MEDLINE=93129188; PubMed=1482345;
 RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
 RT "A tryptophan-substituted member of the AKH/RCH family isolated from
 RT a stick insect corpus cardiaca.";
 RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
 CC -1- FUNCTION: HYPERTREHALOSEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH OF INSECTS.
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS IS
 CC -1- MASS SPECTROMETRY: MM=1308.61; METHOD-FAB.
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTII / RCH FAMILY.
 DR PIR: S07157; S07157.
 DR PIR: S09138; S09138.
 DR Interpro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Glycoprotein.
 FT MOD_RES 1 1
 FT CARBOHYD 8 8
 FT MOD_RES 10 10
 FT SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;

Query Match 20.0%; Score 11; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.7e+04;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 KLVF 7
 DB 1 QLVF 4

RESULT 44
 HTF_HELZE STANDARD; PRT; 10 AA.
 AC P16353;
 DT 01-AUG-1990 (Rel. 15, Created)


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RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR: G37196; G37196.
KM Hypotensive agent; Venom.
FT MOD_RES 1
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 18.2%; Score 10; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 OK 4
DB 1 OK 2

RESULT 48
ACI_THUAI STANDARD; PRT; 8 AA.
ID ACI_THUAI
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Angiotensin-converting enzyme inhibitor
OS Thunnus albacares (Yellowfin tuna) (Neochannus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Acanthomorpha; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Scombridae; Acanthopterygii; Perciformes; Scombroidei;
OC NCBI_Taxid=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
RT muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR: A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 18.2%; Score 10; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HQ 4
DB 3 HIK 5

RESULT 49
AL11_CYPDO STANDARD; PRT; 8 AA.
ID AL11_CYPDO
AC P82152;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Cydiastatin 1.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_Taxid=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";

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RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
CC Neuropeptide; Amidation.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 934 MW; C82879CA5B51F775 CRC64;

Query Match 18.2%; Score 10; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HH 2
DB 3 HY 4

RESULT 50
ICK8_LEDMA STANDARD; PRT; 8 AA.
ID ICK8_LEDMA
AC P19990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE Leucokinin VIII (L-VIII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberidae; Blaberidae; Leucophaea.
OX NCBI_Taxid=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RT VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -1- FUNCTION: THIS CEPHALOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
CC PIR: JS0318; JS0318.
DR PIR: JS0318; JS0318.
KM Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 902 MW; 736365AB59CADD8 CRC64;

Query Match 18.2%; Score 10; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 FFA 9
DB 4 FYS 6

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Search completed: October 29, 2002, 09:37:57
 Job time : 13 secs

RESULT 2
 09GD36 PRELIMINARY; PRT; 9 AA.
 ID 09GD36
 AC 09GD36
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE RIBOSOMAL PROTEIN S16 (FRAGMENT).
 GN RPS16.
 OS Juncus effusus.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Juncaceae; Juncus.
 NCBI_TaxID=13579;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RA Amussen C.B., Chase M.W.;
 RT "Coding and noncoding plastid DNA in palm systematics.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ04962; CAC17904.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1135 MW; 8DCCC9D2C046CB41 CRC64;

Query Match 34.5%; Score 19; DB 8; Length 9;
 Best Local Similarity 60.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLVFF 8
 Db 4 QIVFF 8
 RESULT 3
 0924N8 PRELIMINARY; PRT; 9 AA.
 ID 0924N8
 AC 0924N8
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE NIEMANN PICK TYPE C1 PROTEIN (FRAGMENT).
 GN NPC1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Gevry N.Y., Lacroix D.A., Murphy B.D.;
 RT "Niemann-Pick C1 protein gene, partial cds and promoter region."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF184964; AA83683.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 890 MW; 2C4E2DC761E1EDD8 CRC64;

Query Match 32.7%; Score 18; DB 11; Length 9;
 Best Local Similarity 60.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HHOKL 5
 Db 4 HHPAL 8
 RESULT 4
 039952 PRELIMINARY; PRT; 10 AA.
 ID 039952
 AC 039952

DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE E1 PROTEIN (FRAGMENT).
 OS Hepatitis GB virus C.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC GBV-C/HGV group.
 NCBI_TaxID=39839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ED-INBURNH HAEMOPHILIC;
 RX MEDLINE=97368412; PubMed=9225026;
 RA Smith D.B., Cuccane N., Davidson F., Jarvis L.M., Mokili J.L.,
 RA Hamid S., Ludlam C.A., Simmonds P.;
 RT "Discrimination of hepatitis G virus/GBV-C geographical variants by
 RT analysis of the 5' non-coding region."
 RL J. Gen. Virol. 78:1533-1542(1997).
 DR EMBL: AF003170; AAC57981.1; -.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1152 MW; CC88F0C9C7272732 CRC64;

Query Match 30.9%; Score 17; DB 12; Length 10;
 Best Local Similarity 75.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 LVFF 8
 Db 5 LIFFF 8
 RESULT 5
 09WLE4 PRELIMINARY; PRT; 10 AA.
 ID 09WLE4
 AC 09WLE4
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE POLYPROTEIN (FRAGMENT).
 OS Hepatitis G virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC GBV-C/HGV group.
 NCBI_TaxID=45255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SG3403;
 RX MEDLINE=9926693; PubMed=10335862;
 RA Wong S.B.-J., Chan S.H., Ren E.C.;
 RT "Diversity of GB virus C/hepatitis G virus isolates in Singapore:
 RT predominance of group 2a and the Asian group 3 variant."
 RL J. Med. Virol. 58:145-153(1999).
 DR EMBL: AF078063; AAC32369.1; -.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1152 MW; CC88F0C9C7272732 CRC64;

Query Match 30.9%; Score 17; DB 12; Length 10;
 Best Local Similarity 75.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 LVFF 8
 Db 5 LIFFF 8
 RESULT 6
 P82070 PRELIMINARY; PRT; 5 AA.
 ID P82070
 AC P82070
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE RUBELIDIN 1.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN SECRETION;
 RA Steinborner S.T., Mabitiz P.A., Waugh R.J., Bowie J.H., Gao C.,
 Tyler M.J., Wallace J.C.,
 RT "The structure of new peptides from the Australian red tree frog
 'Litoria rubella', the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 ANTI-BIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=598; METHOD=FAB.
 KM Amphibian skin.
 SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;
 Query Match 29.1%; Score 16; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 FFA 9
 DB 3 FFA 5
 RESULT 7
 P82071 PRELIMINARY; PRT; 5 AA.
 AC P82071;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE RUBELIDIN 2.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-SKIN SECRETION;
 RA Steinborner S.T., Mabitiz P.A., Waugh R.J., Bowie J.H., Gao C.,
 Tyler M.J., Wallace J.C.,
 RT "The structure of new peptides from the Australian red tree frog
 'Litoria rubella', the skin peptide profile as a probe for the study
 of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 ANTI-BIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=626; METHOD=FAB.
 KM Amphibian skin.
 SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CAB10300000 CRC64;
 Query Match 29.1%; Score 16; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 7 FFA 9
 DB 3 FFA 5
 RESULT 8
 O15894 PRELIMINARY; PRT; 8 AA.
 ID O15894;
 AC O15894;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE (CLONE XP587B) (FRAGMENT).
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinnault C.A., Baldwin A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.,
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 arrayed cDNAs and cosmid libraries.";
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL; L32074; AAA73884.1.
 FT NON_TER 1 8
 FT 1 8
 SQ SEQUENCE 8 AA; 952 MW; EBC735B1E1F1B6D6 CRC64;
 Query Match 29.1%; Score 16; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.6e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HH 2
 DB 4 HH 5
 RESULT 9
 O40530 PRELIMINARY; PRT; 8 AA.
 ID O40530;
 AC O40530;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
 DE P20 N WITH A LEADER PEPTIDE.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87089808; PubMed=3540612;
 RA Herman L.M.F., Montagu M.C.V., Depicker A.G.,
 RT "Isolation of tobacco DNA segments with plant promoter activity.";
 RL Mol. Cell. Biol. 6:4486-4492(1986).
 DR EMBL; M14685; AAA34090.1;
 SQ SEQUENCE 8 AA; 1109 MW; E257205B19C9C9C6 CRC64;
 Query Match 29.1%; Score 16; DB 10; Length 8;
 Best Local Similarity 60.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 6 VFFAE 10
 DB 1 MFFFE 5
 RESULT 10
 O47556 PRELIMINARY; PRT; 9 AA.
 ID O47556;
 AC O47556;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE ASPARTATE TRANSCARBAMOYLASE REGULATORY CHAIN (FRAGMENT).
 GN PYR.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-82275057; PubMed-7051000;
 RA Paza C.D., Karels M.J., Navre M., Schachman H.K.;
 RT "Genes encoding Escherichia coli aspartate transcarbamoylase: The
 RL PYR-PYR operon.";
 RM Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982).
 RN [2]
 RP SEQUENCE OF 1-5 FROM N.A.
 RX MEDLINE-83195078; PubMed-6302686;
 RA Hoover T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Benclini D.A.,
 RD Wild J.R.;
 RT "Nucleotide sequence of the structural gene (pyrB) that encodes the
 RL catalytic polypeptide of aspartate transcarbamoylase of Escherichia
 coli.";
 RM Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).
 RN EMBL: J01670; AAA24475.1; -.
 DR EMBL: J01670; AAA24475.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1085 MW; 99EFD723344AALF1 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HKXL 5
 DB 3 HDNKL 7

RESULT 11

ID 09H4M6 PRELIMINARY; PRT; 9 AA.
 AC 09H4M6;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE PA2 (FRAGMENT).
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD;
 RA Pentecost B.T., Ling G.;
 RT "The human pregnane X receptor promoter complex provides
 RL transcriptional starts for a number of PKR related transcripts.";
 DR EMBL: AY007189; AAG23345.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1129 MW; 82F8E1F1B411B2D1 CRC64;

Query Match 29.1%; Score 16; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5.6e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HH 2
 DB 7 HH 8

RESULT 12

ID 09R5L7 PRELIMINARY; PRT; 8 AA.
 AC 09R5L7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE 1,4-BETA-D-GLUCAN GLUCANOHYDROLASE (EC 3.2.1.4) (FRAGMENT).
 RN Clostridium thermocellum.
 OS Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1515;
 RT

RN [1]
 RP SEQUENCE.
 RX MEDLINE-92231850; PubMed-1567379;
 RA Romanec M.P., Fauth U., Kobayashi T., Huskisson N.S., Barker P.J.,
 RA Demain A.L.;
 RT "Purification and characterization of a new endoglucanase from
 RL Clostridium thermocellum.";
 RM Biochem. J. 283:69-73(1992).
 RN [2]
 RP SEQUENCE 8 AA; 823 MW; C2C1AB1D9D1B775 CRC64;

Query Match 27.3%; Score 15; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 FAE 10
 DB 4 FAE 6

RESULT 13

ID 013591 PRELIMINARY; PRT; 8 AA.
 AC 013591;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE ORF YNL337W (FRAGMENT).
 RN YNL337W;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Obermaier B., Piravandi E., Rinke M.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z71612; CA96271.2; -.
 DR SGD: S0005281; YNL337W.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 1005 MW; SCA441E449C9C720 CRC64;

Query Match 27.3%; Score 15; DB 3; Length 8;
 Best Local Similarity 50.0%; Pred. No. 5.6e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 LVFF 8
 DB 1 LVFF 4

RESULT 14

ID 015889 PRELIMINARY; PRT; 8 AA.
 AC 015889;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE (CLONE XP15HB8) (FRAGMENT).
 RN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coulbough M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of

RT arrayed cDNAs and cosmid libraries.";
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL: U32070; AAA73879.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 865 MW; 0474472325A761E7 CRC64;

Query Match
 Best Local Similarity 27.3%; Score 15; DB 4; Length 8;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HHOKL 5
 Db 2 HPSKL 6

RESULT 15

ID 030790 PRELIMINARY; PRT; 9 AA.
 AC 030790;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DE 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE STREPTOMYCIN RESISTANCE PROTEIN A (FRAGMENT).
 GN STRA.
 OS Erwinia amylovora.
 OC Plasmid pBa8.7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Erwinia.
 OX NCBI_TaxID=552;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CA3R;
 RX MEDLINE-98027397; PubMed-9361446;
 RA Palmer E.L., Tevlotdale B.L., Jones A.L.;
 RT "A relative of the broad-host-range plasmid RSF1010 detected in
 RL Appl. Environ. Microbiol. 63:4604-4607(1997).
 DR EMBL: AF017389; AAC45877.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1099 MW; 0140C9C05451B404 CRC64;

Query Match
 Best Local Similarity 27.3%; Score 15; DB 2; Length 9;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 VFF 8
 Db 6 IFF 8

RESULT 16

ID 046179 PRELIMINARY; PRT; 9 AA.
 AC 046179;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CHLORAMPHENICOL ACETYLTANSFERASE.
 GN CATO.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CW 531;
 RX MEDLINE-9124774; PubMed-2039197;
 RA Bannam T.L., Rood J.I.;
 RT "The relationship between the Clostridium perfringens cat gene
 product and chloramphenicol acetyltransferases from other bacteria.";
 RL Antimicrob. Agents Chemother. 35:471-476(1991).

DR EMBL: M55620; AAA23214.1; -.
 KW Transferase.
 SQ SEQUENCE 9 AA; 1041 MW; AFF4D72322CDD696 CRC64;

Query Match
 Best Local Similarity 27.3%; Score 15; DB 2; Length 9;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 KLVF 7
 Db 6 KLVF 9

RESULT 17

ID 09TT77 PRELIMINARY; PRT; 9 AA.
 AC 09TT77;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE WILM'S TUMOR PROTEIN 1 (FRAGMENT).
 GN WT1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21015404; PubMed-11130975;
 RA Brouillette J.A., Andrew J.R., Venta P.J.;
 RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
 RL Mamm. Genome 11:1079-1086(2000).
 DR EMBL: AF202074; AAF20919.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1231 MW; 58DDF41416D1F403 CRC64;

Query Match
 Best Local Similarity 27.3%; Score 15; DB 6; Length 9;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 HQR 4
 Db 4 HQR 6

RESULT 18

ID 092766 PRELIMINARY; PRT; 9 AA.
 AC 092766;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE FUSION PROTEIN (FRAGMENT).
 GN F.
 OS canine distemper virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
 OX NCBI_TaxID=11232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DOG #5526/89;
 RA Liemann H., Harder T., Haas L.;
 RT "Genetic analysis of the central untranslated genome region and the
 RT proximal coding part of the F gene of wild-type and vaccine distemper
 RL morbilliviruses.";
 DR EMBL: AF026237; AAC09167.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;

Query Match 27.3%; Score 15; DB 12; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HOKL 5
ID 1 1
DB 2 HNKI 5

RESULT 19

Q9RJ78 PRELIMINARY; PRT; 10 AA.
AC Q9RJ78;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE VACUOLATING CYTOTOXIN (FRAGMENT).
GN VACA.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-KOBE 500;
RA Shirasaka D.;
RT "Helicobacter pylori vaca gene, strain Kobe 500, partial cds."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB017599; BAA33412.1; -.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1018 MW; 414390C76879CDD7 CRC64;

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KLVF 7
ID 1 1
DB 2 KLVF 5

RESULT 20

Q9UCS3 PRELIMINARY; PRT; 10 AA.
AC Q9UCS3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE TROPOMYOSIN-3 KDA CALCIUM BINDING PROTEIN FRAGMENT D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC MEDLINE=92090441; PubMed=1836432;
RA Crabos M., Yamakado T., Heizmann C.W., Cerletti N., Buhler F.R.,
RA Erne P.;
RT "The calcium binding protein tropomyosin in human platelets and
RT rat cardiac tissue: elevation in hypertensive cardiac hypertrophy."
RL Eur. J. Clin. Invest. 21:472-478(1991).
SQ SEQUENCE 10 AA; 1126 MW; 7A44FD3DC2DFAEB CRC64;

Query Match 27.3%; Score 15; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FAE 10
ID 1 1
DB 1 FAE 3

RESULT 21
P82223 PRELIMINARY; PRT; 10 AA.
ID P82223;
AC P82223;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE (FRAGMENT).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RC STRAIN-XINZHANG X KEMING; TISSUE-BODY WALL, AND FAT BODY;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of
RT silkworm."
RL I Chuan Hsueh Pao 28:217-224(2001).
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1054 MW; D0F722C325B1F1B2 CRC64;

Query Match 27.3%; Score 15; DB 5; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HOKLV 6
ID 1 1
DB 5 HSKVL 9

RESULT 22

P82224 PRELIMINARY; PRT; 10 AA.
ID P82224;
AC P82224;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE (FRAGMENT).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RC STRAIN-XINZHANG X KEMING; TISSUE-BODY WALL, AND FAT BODY;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of
RT silkworm."
RL I Chuan Hsueh Pao 28:217-224(2001).
FT NON_TER 10 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1054 MW; D77CBF25B1F1B2CD CRC64;

Query Match 27.3%; Score 15; DB 5; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 HOKLV 6
ID 1 1
DB 6 HSKVL 10

RESULT 23

Q9UMH9 PRELIMINARY; PRT; 8 AA.
ID Q9UMH9;
AC Q9UMH9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE RHCE PROTEIN (FRAGMENT).
 GN RHCE.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD.
 RX MEDLINE=97260406; PubMed=9106526;
 RA Matsui G., Cherif-Zahar B., Mouro I., Cartton J.P.;
 RT "Characterization of the recombination hot spot involved in the
 RT genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
 RT phenotype.";
 RL Am. J. Hum. genet. 60:808-817(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD.
 RX MEDLINE=90349591; PubMed=1696722;
 RA Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P.,
 RT "Molecular cloning and protein structure of a human blood group Rh
 RT polypeptide.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6243-6247(1990).
 DR EMBL; 297030; CAB09726.1; -.
 FT NON_TER
 FT SEQUENCE 8 AA; 1049 MW; C007244691FB5AB1 CRC64;

Query Match 25.5%; Score 14; DB 4; Length 8;
 Best Local Similarity 40.0%; Pred. No. 5.6e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HHOKL 5
 DB 3 YHML 7

RESULT 24
 ID 09UC36 PRELIMINARY; PRT; 9 AA.
 AC 09UC36;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE 28 KDA HEAT SHOCK PROTEIN HOMOLOGY FRAGMENT 1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92218434; PubMed=1560006;
 RA Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
 RT "Copurification of small heat shock protein with alpha B crystallin
 RT from human skeletal muscle.";
 RL J. Biol. Chem. 267:7718-7725(1992).
 SQ SEQUENCE 9 AA; 1220 MW; 26933415B1F7B43 CRC64;

Query Match 25.5%; Score 14; DB 4; Length 9;
 Best Local Similarity 50.0%; Pred. No. 5.6e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 HOKL 5
 DB 5 HSRL 8

RESULT 25
 ID 094VG2 PRELIMINARY; PRT; 9 AA.
 AC 094VG2;
 DT 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
 GN COI.
 OS Varanus indicus.
 CC Mitochondrion.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosaurs; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
 OX NCBI_TaxID=62043;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidae (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL; AF407505; AAL10069.1; -.
 FT NON_TER
 FT SEQUENCE 9 AA; 1258 MW; 881259C727336411 CRC64;

Query Match 25.5%; Score 14; DB 8; Length 9;
 Best Local Similarity 50.0%; Pred. No. 5.6e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 LVFF 8
 DB 5 LVFF 8

RESULT 26
 ID P82937 PRELIMINARY; PRT; 10 AA.
 AC P82937;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE UNKNOWN ENDOSPERM PROTEIN B (FRAGMENT).
 OS Hordeum vulgare (Barley).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 CC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. BOWI; TISSUE=STARCHY ENDOSPERM;
 RX MEDLINE=21088911; PubMed=11271488;
 RA Kristoffersen H.E., Flengsrud R.;
 RT "Separation and characterization of basic barley seed proteins.";
 RL Electrophoresis 21:3693-3700(2000).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 8.5-9.0, ITS MW IS: 11.9 KDA.
 FT NON_TER
 FT SEQUENCE 10 AA; 1297 MW; 8248A50B11FB5EBA CRC64;

Query Match 25.5%; Score 14; DB 10; Length 10;
 Best Local Similarity 25.0%; Pred. No. 2.2e+04;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOK 4
 DB 5 YHER 8

RESULT 27
 ID 009258 PRELIMINARY; PRT; 8 AA.
 AC 009258;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE NIFH (FRAGMENT).
 GN NIFH.
 CC Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanobacteria PCC 8801).
 CC Bacteria; Cyanobacteria; Chroococcales; Cyanophyceae.

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OX NCB1_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RF-1;
RX MEDLINE=99231861; PubMed=10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
RT "Organization and expression of nitrogen-fixation genes in the aerobic
RT nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
RT RF-1."
RL Microbiology 145:743-753(1999).
DR EMBL, AF001780; AAC33369.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;

Query Match
Best Local Similarity 23.6%; Score 13; DB 2; Length 8;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 OKLVEF 8
Db 2 RQIAFY 7

RESULT 28
Q9S6D5 PRELIMINARY; PRT; 8 AA.
ID Q9S6D5
AC Q9S6D5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PUTATIVE IS30 TRANSPOSASE (FRAGMENT).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCB1_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A295B;
RX MEDLINE=99194747; PubMed=10094716;
RA Kahn A., Drummeismitz J., Whitfield C.;
RT "Conserved organization in the cps gene clusters for expression of
RT biosynthesis locus and the cps genes from Klebsiella pneumoniae."
RT J. Bacteriol. 181:2307-2313(1999).
DR EMBL, AF18251; AAD30008.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 1011 MW; F21DC1A9D1B41406 CRC64;

Query Match
Best Local Similarity 23.6%; Score 13; DB 2; Length 8;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 FFEE 10
Db 5 FTAE 8

RESULT 29
Q56759 PRELIMINARY; PRT; 8 AA.
ID Q56759
AC Q56759;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HALOACID DEHALOGENASE (FRAGMENT).
GN DHAL.
OS Xanthobacter autotrophicus.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Hyphomicrobium group; Xanthobacter.
OX NCB1_TaxID=280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GJ10, AND CV. M50;

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RX MEDLINE=95173113; PubMed=7868610;
RA Van der Ploeg J., Willemsen M., Van Hall G., Janssen D.B.;
RT "Adaptation of Xanthobacter autotrophicus GJ10 to bromoacetate due to
RT activation and mobilization of the haloacetate dehalogenase gene by
RT insertion element IS1247."
RL J. Bacteriol. 177:1348-1356(1995).
DR EMBL, X84038; CAA58857.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 922 MW; F3A9D2D2CDD33056 CRC64;

Query Match
Best Local Similarity 23.6%; Score 13; DB 2; Length 8;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KLVEF 8
Db 3 KAYVF 7

RESULT 30
Q9UDZ4 PRELIMINARY; PRT; 8 AA.
ID Q9UDZ4
AC Q9UDZ4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RHD PROTEIN (FRAGMENT).
GN RHD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE=97260406; PubMed=9106526;
RA Matsui G., Cherif-zahar B., Mouro I., Cartton J.P.;
RT "Characterization of the recombination hot spot involved in the
RT genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
RT phenotype."
RL Am. J. Hum. Genet. 60:808-817(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE=93066356; PubMed=1438298;
RA Le Van Kim C., Mouro I., Cherif-zahar B., Raynal V., Cherrier C.,
RA Cartton J.P., Collin Y.;
RT "Molecular cloning and primary structure of the human blood group Rh
RT polypeptide."
RL Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929(1992).
DR EMBL, Z97031; CAB09727.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 1042 MW; D296944691F85A81 CRC64;

Query Match
Best Local Similarity 23.6%; Score 13; DB 4; Length 8;
Matches 1; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HHOKIV 6
Db 3 YHANNM 8

RESULT 31
Q15899 PRELIMINARY; PRT; 8 AA.
ID Q15899
AC Q15899;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 12D3 ANTIGEN (FRAGMENT).
GN B012D3.

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OS Babesia ovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5869;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ANKARA;
RA Silas G.U., Blakeley R.L., Riddles P.W.;
RT "Characterization of the transcriptional control region of the 12D3
  antigen gene from the sporozoan Babesia bovis."
  Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U44919; AAB6365.1;
FT NON-TER
SQ SEQUENCE 8 AA; 992 MW; F0C7273411B2C726 CRC64;

Query Match      23.6%; Score 13; DB 5; Length 8;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 KLVF 7
DB 5 RLFF 8

RESULT 32
O9GMH3 PRELIMINARY; PRT; 8 AA.
ID 09GMH3
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ACTIN (FRAGMENT).
OS Lagenorhynchus obscurus (dusky dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagenorhynchus.
OX NCBI_TaxID=27611;
RN (1)
RP SEQUENCE FROM N.A.
RA Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
  Speciation, Systematics and Conservation."
  Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140833; AAF98686.1;
FT NON-TER
SQ SEQUENCE 8 AA; 962 MW; 5BD1F417740862C0 CRC64;

Query Match      23.6%; Score 13; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HQ 3
DB 7 HQ 8

RESULT 33
O28866 PRELIMINARY; PRT; 8 AA.
ID 028866
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE ACTIN PROTEIN (FRAGMENT).
OS Megaptera novaeangliae (Humpback whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaeonopteridae; Megaptera.
OX NCBI_TaxID=9773;
RN (1)
RP SEQUENCE FROM N.A.
DR MEDLINE=94285813; PubMed=7912407;

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RA Palumbi S.R., Baker C.S.;
RT "Contrasting population structure from nuclear intron sequences and
  mtDNA of humpback whales."
  Mol. Biol. Evol. 11:426-435(1994).
DR EMBL; S73467; AAD14118.1;
FT NON-TER
SQ SEQUENCE 8 AA; 906 MW; 69C866D1F4177408 CRC64;

Query Match      23.6%; Score 13; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HQ 3
DB 5 HQ 6

RESULT 34
O02831 PRELIMINARY; PRT; 8 AA.
ID 002831
AC 002831;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=96377339; PubMed=8783186;
RA Metaranta M., Kujala U.M., Pellinleht L., Osterman H., Aho H.,
  Vuorio E.;
RT "Evidence for insufficient chondrocytic differentiation during repair
  of full-thickness defects of articular cartilage."
  Matrix Biol. 15:39-47(1996).
DR EMBL; S83371; AAD14433.1;
FT NON-TER
SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match      23.6%; Score 13; DB 6; Length 8;
Best Local Similarity 42.9%; Pred. No. 5.6e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 HQKLVF 7
DB 1 HWPCLLF 7

RESULT 35
O99NX9 PRELIMINARY; PRT; 8 AA.
ID 099NX9
AC 099NX9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID BETA PROTEIN (FRAGMENT).
OS Hydrochoerus hydrochaeris (Capybara) (Carpincho).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognath; Hydrochaeridae;
OC Hydrochaeris.
OX NCBI_TaxID=10149;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Elstirk E., Johnson W.E., Zhang Y.P., Ryder O.A.;
RT "Molecular phylogenetics and the origins of placental mammals."
  Nature 409:614-618(2001).
DR EMBL; AY011342; AAC47377.1;

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FT NON_TER 1 1
SQ SEQUENCE 8 AA; 1071 MW; 1356868DB19C9C3 CRC64;
Query Match 23.6%; Score 13; DB 11; Length 8;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 FFAE 10
11;
DB 2 FFEQ 5

RESULT 36
ID O15891 PRELIMINARY; PRT; 9 AA.
AC O15891;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE (CLONE XP2EBB) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACEITA;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coulbough M.I., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries";
RT Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32131; AAA73881.1; -;
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 1030 MW; E56635A1A33686D1 CRC64;

Query Match 23.6%; Score 13; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HQ 3
11
DB 2 HQ 3

RESULT 37
ID O9GJV3 PRELIMINARY; PRT; 9 AA.
AC O9GJV3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ACTIN (FRAGMENT).
OS Lagorhynchus obscurus (dusky dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagorhynchus.
OX NCBI_TaxID=27611;
RN [1]
RP SEQUENCE FROM N.A.
RA Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT Speciation, Systematics and Conservation";
RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140834; AAF98687.1; -;
DR EMBL; AF140832; AAF98685.1; -;
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1049 MW; ID0EF417740862C0 CRC64;
Query Match 23.6%; Score 13; DB 6; Length 9;

Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HQ 3
11
DB 8 HQ 9

RESULT 38
ID O9GJV2 PRELIMINARY; PRT; 9 AA.
AC O9GJV2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ACTIN (FRAGMENT).
OS Lagorhynchus obliquidens (Pacific white-sided dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagorhynchus.
OX NCBI_TaxID=90247;
RN [1]
RP SEQUENCE FROM N.A.
RA Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT Speciation, Systematics and Conservation";
RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140831; AAF98684.1; -;
DR EMBL; AF140826; AAF98679.1; -;
DR EMBL; AF140827; AAF98680.1; -;
DR EMBL; AF140828; AAF98681.1; -;
DR EMBL; AF140829; AAF98682.1; -;
DR EMBL; AF140830; AAF98683.1; -;
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 1049 MW; ID0EF417740862C0 CRC64;

Query Match 23.6%; Score 13; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HQ 3
11
DB 8 HQ 9

RESULT 39
ID O9GJV1 PRELIMINARY; PRT; 9 AA.
AC O9GJV1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ACTIN (FRAGMENT).
OS Lagorhynchus acutus (Atlantic white-sided dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagorhynchus.
OX NCBI_TaxID=90246;
RN [1]
RP SEQUENCE FROM N.A.
RA Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT Speciation, Systematics and Conservation";
RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140825; AAF98678.1; -;
DR EMBL; AF140822; AAF98675.1; -;
DR EMBL; AF140823; AAF98676.1; -;
DR EMBL; AF140824; AAF98677.1; -;
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1049 MW; ID0EF417740862C0 CRC64;

Query Match 23.6%; Score 13; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HQ 3
Db 8 HQ 9

RESULT 40

O9T688 PRELIMINARY; PRT; 9 AA.
AC O9T688;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Gecko gecko (Tokay gecko).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.
OX NCBI_TaxID=36310;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99343618; PubMed=10413626;
RA Macey J.R., Wang Y., Ananjeva N.B., Larson A., Papenfuss T.J.;
RT "Variant patterns of fragmentation among gekkonid lizards of the
genus *Tarantulus* produced by the Indian collision: A molecular
phylogenetic perspective and an area cladogram for central asia.",
RL Mol. Phylogenet. Evol. 12:320-332(1999).
DR EMBL: AF114249; AAD51600.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 9 AA; 1188 MW; 428CB9C9D36411A7 CRC64;

Query Match 23.6%; Score 13; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
Db 6 FFS 8

RESULT 41

O9T4P9 PRELIMINARY; PRT; 10 AA.
AC O9T4P9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Liolaemus darwini.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
OX NCBI_TaxID=109408;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SDS03477; AND SDS03472;
RA Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
RT "Phylogenetic Relationships in the Iguanid Lizard Genus *Liolaemus*:
Multiple Origins of Viviparous Reproduction and a Phylogenetic
Evolution of Andean Vicariance.",
RL Biol. J. Linn. Soc. Lond. 0:0-0(2000).
DR EMBL: AF099274; AAF18928.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 10 AA; 1288 MW; 1A3580C9D3640440 CRC64;

Query Match 23.6%; Score 13; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.5e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
Db 7 FFS 9

RESULT 42

O9ZYV3 PRELIMINARY; PRT; 10 AA.
AC O9ZYV3;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Diposaurus dorsalis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Diposaurus.
OX NCBI_TaxID=51217;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99162288; PubMed=10051389;
RA Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT "Molecular tests of phylogenetic taxonomies: A general procedure and
example using four subfamilies of the lizard family Iguanidae.",
RL Mol. Phylogenet. Evol. 10:367-376(1998).
DR EMBL: AF049857; AAD02514.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 10 AA; 1275 MW; 1A3580C9D36411A0 CRC64;

Query Match 23.6%; Score 13; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.5e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
Db 7 FFS 9

RESULT 43

O9ZYV0 PRELIMINARY; PRT; 10 AA.
AC O9ZYV0;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Petrosaurus thalassius.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OC Petrosaurus.
OX NCBI_TaxID=81826;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99162288; PubMed=10051389;
RA Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT "Molecular tests of phylogenetic taxonomies: A general procedure and
example using four subfamilies of the lizard family Iguanidae.",
RL Mol. Phylogenet. Evol. 10:367-376(1998).
DR EMBL: AF049858; AAD02517.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 10 AA; 1288 MW; 1A3580C9D3640440 CRC64;

Query Match 23.6%; Score 13; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.5e+04;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
Db 7 FFS 9

RESULT 44

O92YU7 PRELIMINARY; PRT; 10 AA.
ID O92YU7
AC O92YU7
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Sator angustus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Sator.
OX NCBI_TaxID=43619;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99162288; PubMed-10051389;
RA Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT "Molecular tests of phylogenetic taxonomies: A general procedure and
example using four subfamilies of the lizard family Iguanidae.";
RL Mol. Phylogenet. Evol. 10:367-376(1998).
DR EMBL, AF049859; AAD02520.1; -.
KM Mitochondrion.
FT NON_TER
SQ SEQUENCE 10 AA; 1288 MW; 1A3580C9D3640440 CRC64;

Query Match 23.6%; Score 13; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.5e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
Db 7 FFS 9

RESULT 45

O92YU4 PRELIMINARY; PRT; 10 AA.
ID O92YU4
AC O92YU4
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Sceloporus graciosus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OX NCBI_TaxID=43625;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99162288; PubMed-10051389;
RA Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT "Molecular tests of phylogenetic taxonomies: A general procedure and
example using four subfamilies of the lizard family Iguanidae.";
RL Mol. Phylogenet. Evol. 10:367-376(1998).
DR EMBL, AF049860; AAD02523.1; -.
KM Mitochondrion.
FT NON_TER
SQ SEQUENCE 10 AA; 1365 MW; 129780C9D3640440 CRC64;

Query Match 23.6%; Score 13; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.5e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
Db 7 FFS 9

RESULT 46

O92YU1 PRELIMINARY; PRT; 10 AA.
ID O92YU1
AC O92YU1
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Uma scoparia.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Uma.
OX NCBI_TaxID=81829;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99162288; PubMed-10051389;
RA Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT "Molecular tests of phylogenetic taxonomies: A general procedure and
example using four subfamilies of the lizard family Iguanidae.";
RL Mol. Phylogenet. Evol. 10:367-376(1998).
DR EMBL, AF049861; AAD02526.1; -.
KM Mitochondrion.
FT NON_TER
SQ SEQUENCE 10 AA; 1288 MW; 1A3580C9D3640440 CRC64;

Query Match 23.6%; Score 13; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.5e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 FFA 9
11:
Db 7 FFS 9

RESULT 47

O92YT8 PRELIMINARY; PRT; 10 AA.
ID O92YT8
AC O92YT8
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Urosaurus graciosus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
OX NCBI_TaxID=43647;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99162288; PubMed-10051389;
RA Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;
RT "Molecular tests of phylogenetic taxonomies: A general procedure and
example using four subfamilies of the lizard family Iguanidae.";
RL Mol. Phylogenet. Evol. 10:367-376(1998).
DR EMBL, AF049862; AAD02529.1; -.
KM Mitochondrion.
FT NON_TER
SQ SEQUENCE 10 AA; 1288 MW; 1A3580C9D3640440 CRC64;

Query Match 23.6%; Score 13; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.5e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 7 FFS 9

RESULT 48

ID 09ZYS5 PRELIMINARY; PRT; 10 AA.

AC 09ZYS5; 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)

CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).

COI.

Uta stansburiana.

Mitochondrion.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae; Uta.

NCBI_TaxID=43653;

SEQUENCE FROM N.A.

MEDLINE=99162288; PubMed=10051389;

Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;

"Molecular tests of phylogenetic taxonomies: A general procedure and

example using four subfamilies of the lizard family Iguanidae.";

Mol. Phylogenet. Evol. 10:367-376(1998).

EMBL; AF049863; AAD02532.1; -

Mitochondrion.

NON_TER

SEQUENCE 10 AA; 1288 MW; 1A3580C9D3640440 CRC64;

Query Match 23.6%; Score 13; DB 8; Length 10;

Best Local Similarity 66.7%; Pred. No. 3.5e+04;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 49

ID 09ZYS9 PRELIMINARY; PRT; 10 AA.

AC 09ZYS9; 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)

CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).

COI.

Phymaturus somuncurensis.

Mitochondrion.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Phymaturus.

NCBI_TaxID=81831;

SEQUENCE FROM N.A.

MEDLINE=99162288; PubMed=10051389;

Schulte J.A., Macey J.R., Larson A., Papenfuss T.J.;

"Molecular tests of phylogenetic taxonomies: A general procedure and

example using four subfamilies of the lizard family Iguanidae.";

Mol. Phylogenet. Evol. 10:367-376(1998).

EMBL; AF049865; AAD02538.1; -

Mitochondrion.

NON_TER

SEQUENCE 10 AA; 1288 MW; 1A3580C9D3640440 CRC64;

Query Match 23.6%; Score 13; DB 8; Length 10;

Best Local Similarity 66.7%; Pred. No. 3.5e+04;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 50

ID 09TG98 PRELIMINARY; PRT; 10 AA.

AC 09TG98; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).

COI.

Shinisaurus crocodilurus.

Mitochondrion.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Shinisauridae;

NCBI_TaxID=52224;

SEQUENCE FROM N.A.

MEDLINE=99343613; PubMed=10413621;

Macey J.R., Schulte J.A. II, Larson A., Tunlyev B.S., Orlov N.;

Papenfuss T.J.;

"Molecular phylogenetics, trna evolution, and historical biogeography

in anguillid lizards and related taxonomic families.";

Mol. Phylogenet. Evol. 12:250-272(1999).

EMBL; AF085604; AAD51502.1; -

Mitochondrion.

NON_TER

SEQUENCE 10 AA; 1290 MW; 1CEB80C9D36411A0 CRC64;

Query Match 23.6%; Score 13; DB 8; Length 10;

Best Local Similarity 66.7%; Pred. No. 3.5e+04;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: October 29, 2002, 09:38:29
Job time : 26 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 29, 2002, 09:23:26 ; Search time 31 Seconds

(without alignments)
35,830 Million cell updates/sec

Title: US-09-724-842A-27

Perfect score: 55

Sequence: 1 HHQKVFPAE 10

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database :

A.Geneseq_032802:*

- 1: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1983.DAT:*
- 5: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1984.DAT:*
- 6: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1985.DAT:*
- 7: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1986.DAT:*
- 8: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1987.DAT:*
- 9: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1988.DAT:*
- 10: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1989.DAT:*
- 11: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1990.DAT:*
- 12: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1991.DAT:*
- 13: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1992.DAT:*
- 14: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1993.DAT:*
- 15: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1994.DAT:*
- 16: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1995.DAT:*
- 17: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1996.DAT:*
- 18: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgcdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	22	AA846225 Human APP derived
2	55	100.0	15	20	AA849358 Beta-amyloid peptide
3	55	100.0	17	15	AA84703 Beta-amyloid fragm
4	55	100.0	17	22	AA891774 Amyloid beta-prote
5	55	100.0	17	22	AA891807 Amyloid beta-prote
6	55	100.0	17	22	AA848346 Beta-amyloid anti
7	55	100.0	18	21	AA810963 Beta-amyloid precu
8	55	100.0	19	18	AA818882 AEDANS-beta-amylo
9	55	100.0	19	18	AA818881 TFP-beta-amyloid p
10	55	100.0	19	22	AA846201 Human APP A-beta 1
11	55	100.0	19	22	AA849097 Human amyloid beta

12	55	100.0	21	20	AA730941 Human secretase SE
13	55	100.0	24	15	AA852569 Alzheimer's disease
14	55	100.0	26	19	AA847229 Beta-amyloid pepti
15	55	100.0	26	20	AA733408 Human amyloidogeni
16	55	100.0	27	20	AA733409 Human amyloidogeni
17	55	100.0	28	8	AA70594 Sequence of Alzhei
18	55	100.0	28	10	AA890381 Synthetic A4 amylo
19	55	100.0	28	15	AA854702 Beta-amyloid fragm
20	55	100.0	28	15	AA860368 Beta-amyloid (1-28
21	55	100.0	28	16	AA864170 A4-P(1-28) a parti
22	55	100.0	28	16	AA864172 A4-B(1-28) a parti
23	55	100.0	28	16	AA864174 Generic beta amylo
24	55	100.0	28	17	AA864167 Beta-amyloid prote
25	55	100.0	28	20	AA864167 Beta-amyloid prote
26	55	100.0	28	20	AA864167 Beta-amyloid prote
27	55	100.0	28	20	AA864167 Beta-amyloid prote
28	55	100.0	28	22	AA864167 Beta-amyloid prote
29	55	100.0	28	22	AA864167 Beta-amyloid prote
30	55	100.0	28	22	AA864167 Beta-amyloid prote
31	55	100.0	28	22	AA864167 Beta-amyloid prote
32	55	100.0	28	22	AA864167 Beta-amyloid prote
33	55	100.0	28	22	AA864167 Beta-amyloid prote
34	55	100.0	28	22	AA864167 Beta-amyloid prote
35	55	100.0	28	22	AA864167 Beta-amyloid prote
36	55	100.0	28	22	AA864167 Beta-amyloid prote
37	55	100.0	28	22	AA864167 Beta-amyloid prote
38	55	100.0	28	22	AA864167 Beta-amyloid prote
39	55	100.0	28	22	AA864167 Beta-amyloid prote
40	55	100.0	28	22	AA864167 Beta-amyloid prote
41	55	100.0	28	22	AA864167 Beta-amyloid prote
42	55	100.0	28	22	AA864167 Beta-amyloid prote
43	55	100.0	28	22	AA864167 Beta-amyloid prote
44	55	100.0	28	22	AA864167 Beta-amyloid prote
45	55	100.0	28	22	AA864167 Beta-amyloid prote
46	55	100.0	28	22	AA864167 Beta-amyloid prote
47	55	100.0	28	22	AA864167 Beta-amyloid prote
48	55	100.0	28	22	AA864167 Beta-amyloid prote
49	55	100.0	28	22	AA864167 Beta-amyloid prote
50	55	100.0	28	22	AA864167 Beta-amyloid prote

ALIGNMENTS

RESULT 1	AA846225	standard; peptide; 10 AA.
AC	AA846225;	
DT	04-APR-2001	(first entry)
DE	Human APP derived immunogenic peptide #21.	
XX	Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;	
KW	FC receptor mediated phagocytosis; immunogenic response; neuroprotective;	
KW	amyloid precursor protein; Alzheimer's disease.	
OS	Homo sapiens.	
PN	WO200072880-A2.	
XX	07-DEC-2000.	
PF	26-MAY-2000; 2000WO-US14810.	
PR	28-MAY-1999; 99US-0322289.	
PA	(NEUR-) NEURALAB LTD.	
XX	Schenk DB; Bard F; Vasquez NU; Yednock T;	
PI	WPI: 2001-032104/04.	
DR		

Schenk
Yednock

XX Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid
PT specific antibody
XX
XX Disclosure: Figure 19; 143pp; English.
XX
CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have neurotropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease.
CC
SQ Sequence 10 AA;
Query Match 100.0%; Score 55; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHOKLVFAE 10
DB 1 HHOKLVFAE 10
RESULT 2
ID AAW89358 standard; peptide: 15 AA.
AC AAW89358;
XX
DT 02-MAR-1999 (first entry)
DE Beta-amyloid peptide derivative A-beta-11-25.
XX
KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polyneuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; BAP.
XX
OS Homo sapiens
OS Synthesis.
XX
PN US5854204-A.
XX
PD 29-DEC-1998.
XX
PF 14-MAR-1996; 96US-0612785.
XX
PR 14-MAR-1996; 96US-0612785.
PR 14-MAR-1995; 95US-0404831.
PR 07-JUN-1995; 95US-0475579.
PR 27-OCT-1995; 95US-0548998.
XX
PA (PRAE-) PRAECIS PHARM INC.
XX
PI Benjamin H, Chin J, Findels MA, Garnick MB, Geffer ML;
PI Hundal A, Kasman L, Kelley M, Kudasek W, Lee J;
PI Moliniaux S, Musso G, Reed M, Signer ER, Wakefield J;
DR WPI; 1999-094964/08.
XX
PT New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease
XX

PS Claim 6; Column 81-82; 52pp; English.
XX
CC The present invention describes beta-amyloid peptide (BAP) derivatives.
CC The BAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically BAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of BAP to
CC labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation
CC even when BAP is present in molar excess. The present sequence
CC represents a BAP derivative.
CC
SQ Sequence 15 AA;
Query Match 100.0%; Score 55; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHOKLVFAE 10
DB 3 HHOKLVFAE 12
RESULT 3
ID AAR54703 standard; peptide: 17 AA.
AC AAR54703;
XX
DT 15-DEC-1994 (first entry)
DE Beta-amyloid fragment (12-28).
XX
KW Beta-amyloid protein; BAP; Alzheimer's disease; diagnosis.
XX
OS Homo sapiens
XX
PN WO9409364-A.
XX
PD 28-APR-1994.
XX
PF 13-OCT-1993; 93WO-US09772.
XX
PR 13-OCT-1992; 92US-0959251.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Strittmatter WJ;
XX
DR WPI; 1994-151484/18.
XX
PT Immobilised beta-amyloid protein or fragments - used in assays
PT for obtaining prods for use in the diagnosis and treatment of
PT disorders such as Alzheimer's disease.
XX
PS Claim 5; Page 28; 49pp; English.
XX
CC A construct comprising a beta-amyloid protein (BAP) or fragment (asp.
CC the peptides given in AAR54702-03) immobilised on a solid support can be
CC used to detect cpds. which bind to BAP. Binding of proteins in
CC human cerebrospinal fluid proteins were shown to bind to beta-
CC amyloid peptides 1-28 and 12-28. Hydrophobic mimic peptide (12-28)
CC was used as control.
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 55; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHOKLVFAE 10

DB 2 HHOKLVFFAE 11

RESULT 4

ID AAB91774 standard; Peptide: 17 AA.

XX AAB91774;

XX 22-JUN-2001 (first entry)

XX Amyloid beta-protein fragment peptide SEQ ID NO:950.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
OS Synthetic.

XX MO200069900-A2.

XX 23-NOV-2000. *15-8 00-1900*

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thiбаudeau K;

XX WPI: 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

XX Disclosure: Page 504; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 17 AA;

XX Query Match 100.0%; Score 55; DB 22; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 0.00025;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 HHOKLVFFAE 10

XX 2 HHOKLVFFAE 11

RESULT 5

AAB91807
ID AAB91807 standard; Peptide: 17 AA.

XX AAB91807;

XX 22-JUN-2001 (first entry)

XX Amyloid beta-protein fragment peptide SEQ ID NO:983.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
OS Synthetic.

XX MO200069900-A2.

XX 23-NOV-2000. *15-8 00-1900*

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thiбаudeau K;

XX WPI: 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

XX Disclosure: Page 516; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 17 AA;

XX Query Match 100.0%; Score 55; DB 22; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 0.00025;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 HHOKLVFFAE 10

XX 2 HHOKLVFFAE 11

RESULT 6

ID AAB48346 standard; peptide: 17 AA.

XX AAB48346;

DT	20-APR-2001	(first entry)
XX		
DE	Beta-amyloid antigenic peptide (Abeta10-25).	
XX		
KW	Beta-amyloid; neurotrophic; neuroprotective; vaccine; antibody; brain;	
KM	amyloid plaque; Alzheimer's disease; antigen.	
XX		
OS	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
FT	Modified-site	17
FT	/note=	"C-terminal amide"
XX		
XX	W0200077178-A1.	
XX	21-DEC-2000.	
XX		
PF	15-JUN-2000; 2000WO-US16551.	
XX		
XX	16-JUN-1999; 99US-0139408.	
XX		
PA	(BOST-) BOSTON BIOMEDICAL RES INST.	
XX		
PI	Raso V;	
XX		
XX	WPI; 2001-112220/12.	
DR		
PT	New antibodies which catalyze hydrolysis of beta-amyloid at a	
PT	predetermined amide linkage, useful for e.g. sequestering or reducing	
PT	free beta-amyloid in the bloodstream and brain and preventing formation	
PT	of amyloid plaques -	
XX		
XX	Example 1; Fig 3; 82pp; English.	
XX		
CC	The invention relates to an antibody which catalyzes the hydrolysis of	
CC	beta-amyloid at a predetermined amide linkage. The antibodies are useful	
CC	for sequestering free beta-amyloid in the bloodstream of an animal,	
CC	reducing beta-amyloid levels in the brain, preventing formation of	
CC	amyloid plaques, and disaggregating amyloid plaques present in the brain,	
CC	this may be used in treating patients diagnosed with or at risk for	
CC	Alzheimer's disease. The present sequence represents a beta-amyloid	
CC	antigenic peptide made from the central region of beta-amyloid. The	
CC	antibody peptides were designed to be tested for suitability to	
CC	antibody-mediated therapy.	
XX		
XX		
SQ	Sequence	17 AA;
Query Match	100.0%;	Score 55; DB 22; Length 17;
Best Local Similarity	100.0%;	Pred. NO. 0.00025;
Matches 10; Conservative	0;	Mismatches 0; Indels 0; Gaps 0
QY	1 HHOKLVFAE 10	
DB	5 HHOKLVFAE 14	
RESULT 7		
AA10963		
ID	AA10963 standard; protein; 18 AA.	
XX		
XX	AA10963;	
XX		
DT	07-FEB-2001 (first entry)	
XX		
DE	Beta-amyloid precursor protein peptide fragment.	
XX		
XX	APP; amyloid precursor protein; human; alpha-secretase; ADAM 10;	
KW	disintegrin-metalloprotease; protease; neurotrophic; neuroprotective;	
KM	gene therapy; Alzheimer's disease.	
XX		
OS	Unidentified.	
XX		
PN	DE19910108-A1.	

```

XX 21-SEP-2000.
XX PD
XX 08-MAR-1999; 99DE-1010108.
XX PR
XX 08-MAR-1999; 99DE-1010108.
XX PR
XX (FAHR/) FAHRENHOLZ F.
XX PA
XX Fahrenholz F, Postlma R;
XX DR
XX WPI; 2000-588391/56.
XX
XX Recombinant cells, for identifying alpha-secretase active agents and
XX identifying risk factors associated with Alzheimer's disease, comprise
XX amyloid precursor protein and alpha-secretase
XX
XX Example 13; Page 12; 24pp; German.
XX
XX This invention describes a novel recombinant cell comprising recombinant
XX nucleic acids encoding a region of human amyloid precursor protein
XX containing an alpha-secretase cleavage site and a protease or a
XX heterologous RNA coding for a substrate protein and a protease. The
XX invention also describes a recombinant cell, characterized in that it
XX contains recombinant nucleic acids comprising either: (a) a gene for a
XX substrate protein (SP), which comprises a sequence region of 18 amino
XX acids of the human amyloid precursor protein (APP) or a homologous
XX protein, where the sequence region contains the alpha-secretase cleavage
XX site at a reference of 6 residues at the N-terminal and 12 residues at
XX the C-terminal; and (b) a gene for a protease protein (PP), that either
XX comprises a proteolytically active necessary sequence region or a
XX sequence region of the disintegrin metalloprotease ADAM 10 from a cow
XX (Bos taurus), from a human or other mammal or a mutant of this, which
XX shows the same enzymatic properties, where the genes are under the
XX control of heterologous promoters; or a heterologous RNA coding for a SP
XX and a PP. The products of the invention have neurotropic and
XX neuroprotective activity and can be used for gene therapy. The protease
XX proteins of the invention are useful for proteolytic cleavage of
XX substrate proteins, especially human amyloid precursor protein. Dominant
XX negative forms of bovine, human or other mammalian
XX disintegrin-metalloprotease ADAM 10 proteins and their coding sequences
XX are useful for suppressing the alpha-secretase activity of a cell.
XX Nucleic acid sequences encoding the proteases are useful for
XX constructing vectors for gene therapy. The proteins and recombinant cells
XX are useful for identifying secretases and pharmaceutical agents and to
XX identify risk factors associated with Alzheimer's disease.
XX
XX Sequence 18 AA:
XX
XX Query Match 100.0%; Score 55; DB 21; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 0.00027;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 HHOKLVEFAE 10
XX | | | | | | | |
XX 3 HHOKLVEFAE 12
XX
XX RESULT 8
XX AAM18882
XX ID AAM18882 standard; peptide; 19 AA.
XX AC AAM18882;
XX XX
XX DT 08-DEC-1997 (first entry)
XX DE
XX AEDANS-beta-amyloid peptide fragment (9-25).
XX XX
XX beta-amyloid-peptide; membrane protein; amyloid precursor protein;
XX fibril assembly; in vitro; detection; fluorescence; amyloidosis disorder;
XX Alzheimer's disease; multiple myeloma; rheumatoid arthritis; diabetes;
XX prion disorder.
XX KM
XX

```

OS Synthetic.
 XX
 FH Key
 FT Modified-site 1 Location/Qualifiers
 FT Modified-site 1 /note= "AEDANS-Ac-Cys"
 FT Modified-site 19 /note= "Gly-CONH2"
 FT Modified-site 19 /note= "Gly-CONH2"
 XX
 PN MO9707402-A1.
 XX
 PD 27-FEB-1997.
 XX
 PF 16-AUG-1996; 96MO-CA00555.
 XX
 PR 17-AUG-1995; 95US-0515615.
 XX
 PA (ONTA-) ONTARIO CANCER INST.
 XX
 PI Chakrabarty A;
 XX
 DR WPI; 1997-165446/15.
 XX
 PT In vitro fluorescence monitoring of protein fibril assembly - esp.
 PT useful for monitoring fibril assembly processes associated with
 PT amyloidosis disorders, esp. Alzheimer's disease
 XX
 PS Claim 26; Page 25; 40pp; English.
 XX
 CC Beta-amyloid protein fibril assembly can be monitored using a new method
 CC for in vitro monitoring of peptide/protein fibril assembly using
 CC fluorescent energy transfer between closely juxtaposed donor and
 CC acceptor fluorophores. Two forms of beta-amyloid (9-25) were synthesised,
 CC one had a Trp residue attached to the N-terminus of the peptide
 CC (AAW18881), and the other (AAW18882) had a cysteine residue attached to
 CC the N-terminus, and an AEDANS group chemically linked to the sulfhydryl
 CC side chain of the cysteine. When both forms of beta-amyloid are mixed
 CC together, fibrils will assemble and in the fibril state the Trp and
 CC AEDANS groups will be closer in space than in the non-fibril state.
 CC Fluorescence energy transfer between Trp and AEDANS increases when the
 CC two fluorophores are close in space (i.e. efficiency of energy transfer
 CC will increase as the fibrils form) and the fluorescence can be measured.
 CC Fibril assembly processes associated with various amyloidosis disorders
 CC can be monitored by the method, especially Alzheimer's disease (claimed),
 CC multiple myeloma, rheumatoid arthritis, diabetes and prion disorders.
 CC
 XX
 SQ Sequence 19 AA;
 XX
 QY Query Match 100.0%; Score 55; DB 18; Length 19;
 QY Best Local Similarity 100.0%; Pred. No. 0.00029;
 QY Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHOKLVFAE 10
 QY |||||
 QY 7 HHOKLVFAE 16
 DB
 XX
 ID AAW18881 standard; peptide; 19 AA.
 XX
 AC AAW18881;
 XX
 DT 08-DEC-1997 (first entry)
 XX
 DE Trp-Beta-amyloid peptide fragment (9-25).
 XX
 KW beta-amyloid peptide; membrane protein; amyloid precursor protein;
 KW fibril assembly; in vitro; detection; fluorescence; amyloidosis disorder;
 KW Alzheimer's disease; multiple myeloma; rheumatoid arthritis; diabetes;
 KW prion disorder.
 OS
 XX
 OS Synthetic.

FH Key
 FT Modified-site 1 Location/Qualifiers
 FT Modified-site 1 /note= "Acetyl-Trp"
 FT Modified-site 19 /note= "Gly-CONH2"
 FT Modified-site 19 /note= "Gly-CONH2"
 XX
 PN MO9707402-A1.
 XX
 PD 27-FEB-1997.
 XX
 PF 16-AUG-1996; 96MO-CA00555.
 XX
 PR 17-AUG-1995; 95US-0515615.
 XX
 PA (ONTA-) ONTARIO CANCER INST.
 XX
 PI Chakrabarty A;
 XX
 DR WPI; 1997-165446/15.
 XX
 PT In vitro fluorescence monitoring of protein fibril assembly - esp.
 PT useful for monitoring fibril assembly processes associated with
 PT amyloidosis disorders, esp. Alzheimer's disease
 XX
 PS Claim 36; Page 25; 40pp; English.
 XX
 CC Beta-amyloid protein fibril assembly can be monitored using a new method
 CC for in vitro monitoring of peptide/protein fibril assembly using
 CC fluorescent energy transfer between closely juxtaposed donor and
 CC acceptor fluorophores. Two forms of beta-amyloid (9-25) were synthesised,
 CC one had a Trp residue attached to the N-terminus of the peptide
 CC (AAW18881), and the other (AAW18882) had a cysteine residue attached to
 CC the N-terminus, and an AEDANS group chemically linked to the sulfhydryl
 CC side chain of the cysteine. When both forms of beta-amyloid are mixed
 CC together, fibrils will assemble and in the fibril state the Trp and
 CC AEDANS groups will be closer in space than in the non-fibril state.
 CC Fluorescence energy transfer between Trp and AEDANS increases when the
 CC two fluorophores are close in space (i.e. efficiency of energy transfer
 CC will increase as the fibrils form) and the fluorescence can be measured.
 CC Fibril assembly processes associated with various amyloidosis disorders
 CC can be monitored by the method, especially Alzheimer's disease (claimed),
 CC multiple myeloma, rheumatoid arthritis, diabetes and prion disorders.
 CC
 XX
 SQ Sequence 19 AA;
 XX
 QY Query Match 100.0%; Score 55; DB 18; Length 19;
 QY Best Local Similarity 100.0%; Pred. No. 0.00029;
 QY Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHOKLVFAE 10
 QY |||||
 QY 7 HHOKLVFAE 16
 DB
 XX
 ID AAB46201 standard; peptide; 19 AA.
 XX
 AC AAB46201;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human APP A-beta 13-28 peptide.
 XX
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 OS
 XX
 OS Homo sapiens.
 PN MO200072880-A2.
 XX
 PD 07-DEC-2000.

XX	26-MAY-2000; 2000WO-US14810.
PF	
XX	28-MAY-1999; 99US-0322289.
XX	
XX	(NEUR-) NEURALAB LTD.
PA	
XX	Schenk DB, Bard F, Vasquez NJ, Yednock T;
PI	
XX	WPI; 2001-032104/04.
DR	
XX	Preventing or treating a disease associated with amyloid deposits,
PT	especially Alzheimer's disease, comprises administering amyloid
XX	specific antibody -
XX	
PS	Disclosure; Page 61; 143pp; English.
XX	
XX	This invention describes a novel method of preventing or treating a
CC	disease associated with amyloid deposits of amyloid precursor protein
CC	(APP) Abeta fragments in the brain of a patient, which comprises
CC	administering to the patient: (a) an antibody that binds to Abeta, the
CC	antibody binds to an amyloid deposit and induces a clearing response (Fc
CC	receptor mediated phagocytosis) against it (b) a polypeptide containing
CC	an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC	that induces an immunogenic response against residues 1-3 to 7-11 of
CC	Abeta. The products of the invention have neurotropic and neuroprotective
CC	activity. The method is also useful for monitoring a course of treatment
CC	being administered to a patient e.g. active and passive immunization. The
CC	methods are useful for prophylactic and therapeutic treatment of
CC	Alzheimer's disease.
XX	
XX	Sequence 19 AA;
SO	
XX	
XX	Query Match 100.0%; Score 55; DB 22; Length 19;
XX	Best Local Similarity 100.0%; Pred. No: 0.00029;
XX	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 HHQKLVFFAE 10
XX	
DB	1 HHQKLVFFAE 10
XX	
XX	RESULT 11
XX	AAB49097
ID	AAB49097 standard; peptide; 19 AA.
XX	
AC	AAB49097;
XX	
DT	27-MAR-2001 (first entry)
XX	
DE	Human amyloid beta peptide (residues 13-28), SEQ ID NO:33.
XX	
KW	Amyloid disease; amyloid fibril deposition; amyloid plaque;
KW	immunogenic; antibody; vaccine; Alzheimer's disease;
KW	type 2 diabetes; reactive system amyloidosis;
KW	systemic senile amyloidosis; familial amyloid cardiomyopathy;
KW	transmissible spongiform encephalopathy; Creutzfeldt-Jakob disease; Kuru;
KW	haemodialysis-associated beta-2-microglobulin deposition;
KW	amyloid beta peptide.
XX	
OS	Homo sapiens.
XX	
PN	WO200072876-A2.
XX	
PD	07-DEC-2000.
XX	
PF	01-JUN-2000; 2000WO-US15239.
XX	
PR	01-JUN-1999; 99US-0137010.
XX	
PA	(NEUR-) NEURALAB LTD.
XX	
PI	Schenk DB;

```

XX WP1: 2001-070921/08.
XX
XX
XX Pharmaceutical composition comprising immunogen against amyloid
XX component such as fibrin peptide or protein, or antibody against
XX amyloid component useful for treating amyloid diseases or amyloidoses -
XX
XX
XX Example IV; Page 74; 140pp; English.
XX
XX The invention relates to a novel pharmaceutical composition for
XX preventing or treating a disease characterised by amyloid fibril
XX deposits (amyloid plaques) in a patient. The pharmaceutical composition
XX comprises an agent that will induce an immune response against an amyloid
XX component, or an antibody or antibody fragment that binds to an amyloid
XX component. The invention also relates to a method for determining
XX the prognosis of a patient undergoing treatment for an amyloid disorder
XX which involves measuring a patient serum amount of immunoreactivity
XX against a selected amyloid component. A patient serum immunoreactivity
XX of at least four times a base line serum immunoreactivity control level
XX indicates a prognosis of improved status with respect to the disorder.
XX The pharmaceutical compositions of the invention are useful for treating
XX a wide variety of disorders characterised by amyloid fibril deposition in
XX a patient. Such disorders include Alzheimer's disease characterised by
XX amyloid beta peptide fibril deposits; type 2 diabetes characterised by
XX islet amyloid protein peptide (IAPP, amylin) fibrils; reactive systemic
XX amyloidosis associated with systemic inflammatory diseases (e.g.,
XX rheumatoid arthritis, osteomyelitis, tuberculosis); systemic senile
XX fibrils derived from serum amyloid A protein (ApoSAA); systemic senile
XX amyloidosis and familial amyloid cardiomyopathy characterised by ATTR
XX fibrils derived from transthyretin (TTR); transmissible spongiform
XX encephalopathies (e.g. Creutzfeldt-Jakob disease, kuru) characterised by
XX prion protein deposits; and beta-2-microglobulin deposits which form as
XX a result of long term haemodialysis treatment. The present sequence
XX represents a human amyloid beta peptide which was conjugated to
XX sheep anti-mouse IgG in an exemplification of the invention.
XX
XX
XX Sequence 19 Aa:
XX
XX
XX Query Match 100.0%; Score 55; DB 22; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 0.00029;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 HHQKLVFFAE 10
XX ||||||||
XX 1 HHQKLVFFAE 10
XX
XX Db
XX
XX
XX RESULT 12
XX AAY30941
XX ID AAY30941 standard; peptide: 21 Aa.
XX
XX AAY30941;
XX
XX
XX 19-OCT-1999 (first entry)
XX
XX
XX Human secretase SEC-alpha1 peptide fragment.
XX
XX Secretase; hyperforin; treatment; Alzheimer's disease; purification;
XX adhyperforin; St. John's Wort; scorge stable; pharmaceutical;
XX symptom; SEC-alpha1; human.
XX
XX Homo sapiens.
XX
XX WO9941220-A1.
XX
XX 19-AUG-1999.
XX
XX 04-FEB-1999; 99WO-EP00737.
XX
XX 13-FEB-1998; 98DE-1005947.
XX
XX (SCHW-) SCHWADE GMBH & CO WILLMAR.
XX

```


PI Chatterjee SS, Erdelmeier C, Klessing K, Marme D;
PI Schaechele C;
XX
XX
DR WPI; 1999-508609/42.

PT Hyperforin and adhyperforin isolated from St. John's Wort for
PT treatment of Alzheimers

XX
PS Example 34; Fig 1; 43pp; German.

CC This invention describes novel hyperforin and adhyperforin salts of
CC formula (I): (A)^m(B)^p, where m = 1-3; (A)⁻ = an anion of formula (II):
CC n = 0-1; (B)^p = an alkali metal ion or an ammonium ion of a salt-forming
CC nitrogen base of formula (III): R1-R3 = H, an optionally branched alkyl,
CC cycloalkyl, bicycloalkyl, tricycloalkyl, alkenyl, alkynyl,
CC heterocycloalkyl, aryl, heteroaryl, arylalkyl or a heteroarylalkyl group,
CC all optionally substituted with one or more hydroxy, alkoxy, aryloxy,
CC alkenoxy, aroyl, carboxy, alkoxycarbonyl, ureido, amidino, guanidino,
CC cyano, azido, mercapto, alkylthio, alkylsulphoxy, alkylsulphonyl,
CC alkylsulphenyl, aminosulphonyl, fluoro, chloro, bromo, iodo, alkyl or
CC perfluoroalkyl; R1+R2 = together with an N-atom form, together with a
CC N-atom an azetidin-, pyrrolidin-, piperidin-, piperazin-,
CC homopiperazin-, morpholin-, thiomorpholin-, pyridin-, di- or
CC tetra-hydropyridin-, pyrimidin-, pyrazin-, azepin-, diazolin-,
CC oxazepin-, diazepin-, imidazolin-, pyrazol-, oxazol- or thiazol- ring,
CC optionally with aliphatic, heteroaliphatic, aromatic or heteroaromatic
CC rings or substituted with hydroxy, alkoxy, aryloxy, alkanoyl, aroyl,
CC carboxy, alkoxycarbonyl, ureido, amidino, guanidino, cyano, azido,
CC mercapto, alkylthio, alkylsulphoxy, alkylsulphonyl, alkylsulphenyl,
CC aminosulphonyl, fluoro, chloro, bromo, iodo, alkyl or perfluoroalkyl;
CC R4 = H, or an optionally branched alkyl group. The preparation is used to
CC purify the hyperforin and/or adhyperforin content in St. John's Wort
CC extracts. The obtained salts are storage stable and can be used in
CC pharmaceutical compositions for the treatment of Alzheimer's disease and
CC SEC-alpha1 protein which is used to illustrate the method of the
CC invention.

XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 55; DB 20; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
| | | | | | | | | |
DB 8 HHOKLVFFAE 17

RESULT 13

AAR52569
ID AAR52569 standard; peptide; 24 AA.

XX
AC AAR52569;

XX
DT 16-DEC-1994 (first entry)

XX
DE Alzheimer's disease related immunogen.

XX
KW Alzheimer's disease; senile dementia; immunogen.

XX
OS Synthetic.

XX
PN JF06009693-A.

XX
PD 18-JAN-1994.

XX
PE 23-JAN-1992; 92JP-0031341.

XX
PR 23-JAN-1992; 92JP-0031341.

XX
PA (EIKE) EIKEN KAGAKU KK.

DR WPI; 1994-146876/18.

XX
XX Alzheimer's disease related protein isolated from serum of
PT patient - useful in diagnosis

XX
PS Claim 1; Page 2; 8pp; Japanese.

CC A monoclonal antibody raised against the synthetic peptide AAR52569 as
CC immunogen reacts with a new Alzheimer's disease related protein. The
CC novel protein has a mol.wt. of 20kd (by SDS-PAGE), isoelectric point
CC of ca. 5-7 and is abundant in serum of AD patients.

XX
SQ Sequence 24 AA;

Query Match 100.0%; Score 55; DB 15; Length 24;

Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
| | | | | | | | | |
DB 13 HHOKLVFFAE 22

RESULT 14

AAW47229
ID AAW47229 standard; peptide; 26 AA.

XX
AC AAW47229;

XX
DT 22-MAY-1998 (first entry)

XX
DE Beta-amyloid peptide residues 10-35.

XX
KW Screening assay; beta-amyloid peptide; treatment;
KW amyloidosis disease; Alzheimer's disease.

XX
OS Homo sapiens.

XX
PN US5721106-A.

XX
PD 24-FEB-1998.

XX
PE 12-SEP-1994; 94US-0304585.

XX
PR 12-SEP-1994; 94US-0304585.

XX
PR 13-AUG-1991; 91US-0744767.

XX
PA (HARD) HARVARD COLLEGE.

XX
PA (MIND) UNIV MINNESOTA.

XX
PI Maglio JE, Mantyh PW;

XX
DR WPI; 1998-168404/15.

XX
PT New in vitro screening assay for Alzheimer's disease drugs -
PT comprises assessing binding of labelled beta-amyloid peptide to silk
PT sample

XX
PS Claim 8; Columns 31-32; 36pp; English.

CC The present sequence was used in the development of a novel in
CC vitro screening assay for agents capable of affecting the
CC deposition of beta-amyloid peptide (BAP) on tissue. The method
CC comprises contacting a silk sample with labelled BAP, optionally
CC in the presence of a test agent, detecting the amount of label
CC bound to the silk and assessing the effect of the agent on the
CC deposition of BAP. Agents that inhibit binding of BAP to silk are
CC potentially useful for treating amyloidosis diseases, especially
CC Alzheimer's disease.

XX
SQ Sequence 26 AA;

Query Match 100.0%; Score 55; DB 19; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHOKLVFAE 10
DB 4 HHOKLVFAE 13

RESULT 15
AAV33408
ID AAV33408 standard; peptide; 26 AA.

AC AAV33408;

DE 03-DEC-1999 (first entry)

Human amyloidogenic A-beta peptide 2.

KW Amyloidogenic; beta-amyloid; A-beta peptide; human; inhibitor;
KW fibrillogenesis; amyloid plaque; amyloidosis; Alzheimer's disease;
KW Down's Syndrome.

OS Homo sapiens.

PN WO9941279-A2.

PD 19-AUG-1999.

PF 12-FEB-1999; 99WO-US03231.

PR 13-FEB-1998; 98US-0074658.

PA (ARCH-) ARCH DEV CORP.

PI Lynn DG, Meredith SC, Burkoth TS;

DR WPI; 1999-561326/47.

PT Inhibiting amyloid plaque formation in humans suffering from
PT amyloidosis, Alzheimer's disease or Down's Syndrome -

PS Claim 22; Page 140; 141pp; English.

CC This invention describes a novel method for inhibiting amyloid
CC fibrillogenesis which comprises contacting tissue with a composition
CC comprising an amyloidogenic peptide, beta-amyloid, that has been blocked
CC at an end terminal or a side chain, by conjugation to polyethylene
CC glycol, by conjugation to a second compound and a pharmaceutically
CC acceptable buffer, solvent or diluent. The methods are used to inhibit
CC amyloid plaque formation in humans suffering from amyloidosis,
CC Alzheimer's disease or Down's Syndrome. This sequence represents a
CC fragment of the beta-amyloid peptide described in the method of the
CC invention.

SQ Sequence 26 AA;

Query Match 100.0%; Score 55; DB 20; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
DB 4 HHOKLVFAE 13

RESULT 16
AAV33409

ID AAV33409 standard; peptide; 27 AA.

AC AAV33409;

DE 03-DEC-1999 (first entry)

DE Human amyloidogenic A-beta peptide C-terminal fragment.

KW Amyloidogenic; beta-amyloid; A-beta peptide; human; inhibitor;
KW fibrillogenesis; amyloid plaque; amyloidosis; Alzheimer's disease;
KW Down's Syndrome.

OS Homo sapiens.

PN WO9941279-A2.

PD 19-AUG-1999.

PF 12-FEB-1999; 99WO-US03231.

PR 13-FEB-1998; 98US-0074658.

PA (ARCH-) ARCH DEV CORP.

PI Lynn DG, Meredith SC, Burkoth TS;

DR WPI; 1999-561326/47.

PT Inhibiting amyloid plaque formation in humans suffering from
PT amyloidosis, Alzheimer's disease or Down's Syndrome -
PS Disclosure; Page 141; 141pp; English.

CC This invention describes a novel method for inhibiting amyloid
CC fibrillogenesis which comprises contacting tissue with a composition
CC comprising an amyloidogenic peptide, beta-amyloid, that has been blocked
CC at an end terminal or a side chain, by conjugation to polyethylene
CC glycol, by conjugation to a second compound and a pharmaceutically
CC acceptable buffer, solvent or diluent. The methods are used to inhibit
CC amyloid plaque formation in humans suffering from amyloidosis,
CC Alzheimer's disease or Down's Syndrome. This sequence represents the
CC C-terminal fragment of a PEG-derivatized beta-amyloid peptide described
CC in the method of the invention.

SQ Sequence 27 AA;

Query Match 100.0%; Score 55; DB 20; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFAE 10
DB 5 HHOKLVFAE 14

RESULT 17
AAP70594

ID AAP70594 standard; peptide; 28 AA.

AC AAP70594;

DE 15-APR-1991 (first entry)

Sequence of Alzheimer's amyloid polypeptide (AAP).
Diagnosis; Immunologic assay.

OS Homo sapiens.

PN US466829-A.

PD 19-MAY-1987.

PF 15-MAY-1985; 85US-0734660.

PR 15-MAY-1985; 85US-0734660.

PA (REGC) UNIV OF CALIFORNIA.

```

PI    Glennen CG,  Mong CW;
XX
DR    WPI: 1987-157148/22.
XX
PT    Alzheimer's amyloid polypeptide - used for obtaining antibodies
XX    and nucleotide probes for diagnosis of Alzheimer's disease
PS
XX    Claim 1: column 11; 8pp; English.
XX
CC    Brains obtd. from patients suspected of having Alzheimer's disease
CC    and exhibiting extensive cerebrovascular amyloidosis were used for
CC    AAP isolation. The AAP can be used to obtain antibodies which can
CC    be used as reagents (claimed) in a blood or tissue immunologic
CC    assay for the disease. It can also be used to develop a probe
CC    (claimed) which can be used in a diagnostic test (claimed).
XX
SQ    Sequence      28 AA;

Query Match      100.0%; Score 55; DB 8; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy      1 HHOKLVEFAE 10      .
        |||||||
Db      13 HHOKLVEFAE 22

RESULT 18
AAP90381
ID      AAP90381 standard; protein; 28 AA.
XX
AC      AAP90381;
XX
DT      01-NOV-1989 (first entry)
XX
DE      Synthetic A4 amyloid peptide.
XX
KW      Synthetic; A4 amyloid polypeptide; Alzheimer's disease;
XX    Immunossays; antibodies.
OS      Synthetic.
XX
XX      W08906242-A.
XX
PN      13-JUL-1989.
XX
PD      11-OCT-1988; 88WO-US03590.
XX
PE      08-OCT-1987; 87US-0105751.
XX
PR
XX      (MCLE ) MCLEAN HOSPITAL CORP; (UYRO) UNIVERSITY OF ROCHESTER.
PA      Majocha R, Marotta CA, Zain S;
XX      WPI: 1989-220551/30.
XX
DR
XX      Antibodies to A4 amyloid polypeptide
XX      - used in immunossays and for imaging of A4 amyloid
XX      in Alzheimer's diseased patients.
PS
XX      Claim 1; page 27; 30pp; English.
XX
CC      Synthetic A4 amyloid polypeptide (see also AAP90382, AAP90383).
CC      Used as immunogen, (un)coupled, or to produce antibodies. Used in
CC      immunossays and for imaging of A4 amyloid in Alzheimer's disease.
XX
SQ    Sequence      28 AA;

Query Match      100.0%; Score 55; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 HHOKLVEFAE 10

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Db      13 HHOKLVFFAE 22
|||||
RESULT 19
AAR60368
ID AAR64702 standard; peptide: 28 AA.
XX AAR64702;
AC AAR64702;
XX 15-DEC-1994 (first entry)
DT Beta-amyloid fragment (1-28).
XX
DE Beta-amyloid protein; BAP; Alzheimer's disease; diagnosis.
KW Homo sapiens.
XX W09409364-A.
XX 28-APR-1994.
PD 13-OCT-1993; 93WO-US09772.
PE 13-OCT-1992; 92US-0959251.
PR (UYDU-) UNIV DUKE.
XX PA
XX PI
XX STittmatter WJ;
DR WPT; 1994-151484/18.
XX
PX Immobilised beta-amyloid protein or fragments - used in assays
PT for obtaining prods for use in the diagnosis and treatment of
PI disorders such as Alzheimer's disease.
PS Claim 4; Page 28; 49pp; English.
CC
XX A construct comprising a beta-amyloid protein (BAP) or fragment (esp.
CC the peptides given in AAR64702-03) immobilised on a solid support can be
CC used to detect cpds which bind to BAP. Binding of proteins in
CC human cerebrospinal fluid proteins were shown to bind to beta-
CC amyloid peptides 1-28 and 12-28. Hydrophobic mimic peptide (12-28)
CC was used as control.
XX
SQ Sequence 28 AA;
Query Match 100.0%; Score 55; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22
|||
RESULT 20
AAR60368
ID AAR60368 standard; peptide: 28 AA.
XX AAR60368;
AC AAR60368;
XX 15-MAR-1995 (first entry)
DT Beta-amyloid (1-28).
XX
DE Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
KW anti-beta-amyloid antibody; diagnosis; immunogen; antigen; epitope.
XX Homo sapiens.
XX W09417197-A.
XX

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PD 04-AUG-1994.
XX
XX 24-JAN-1994; 94WO-JP00089.
XX
XX 25-JAN-1993; 93JP-0010132.
PR 05-FEB-1993; 93JP-0019035.
PR 16-NOV-1993; 93JP-0286985.
PR 28-DEC-1993; 93JP-0334773.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Kitada C, Odaka A, Suzuki N;
XX
XX WPI; 1994-264110/32.
XX
XX Antibodies recognising specific parts of beta-amyloid - can be
XX used for diagnosis of diseases implicating beta-amyloid, such as
XX Alzheimer's disease
XX
XX Claim 7; Page 84; 116pp; Japanese.
XX
XX Antibodies which recognise specific subfragments of the beta-amyloid
XX protein are claimed. Specifically, the antibodies (which are pref.
XX monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
XX portion of beta-amyloid or they recognise residues 25-35 or 35-43
XX from the C-terminal portion. The antibodies are useful for assaying
XX beta-amyloid and its derivatives for diagnosis of Alzheimer's
XX disease.
XX
XX Sequence 28 AA:
SQ
XX
XX Query Match 100.0%; Score 55; DB 15; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 0.00044;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHOKLVFFAE 10
XX | | | | | | | |
XX 13 HHOKLVFFAE 22
DB
XX
XX RESULT 21
XX AAR64170
XX ID AAR64170 standard; peptide; 28 AA.
XX
XX AAR64170;
XX
XX 03-AUG-1995 (first entry)
XX
XX A4-O(1-28) a partial beta amyloid peptide.
XX
XX beta amyloid protein; mutant; variant; detection; amyloid deposition;
XX diagnosis; amyloidosis associated disease; Alzheimer's disease;
XX Down's syndrome; A4-O(1-28).
XX
XX Synthetic.
XX
XX W09428412-A.
XX
XX 08-DEC-1994.
XX
XX 27-MAY-1994; 94WO-US05809.
XX
XX 28-MAY-1993; 93US-0069010.
XX
XX (MIRI-) MIRIAM HOSPITAL.
XX
XX Majocha RE, Marotta CA;
XX
XX WPI; 1995-023013/03.
XX
XX Amyloid binding composition comprising labelled amyloid protein
XX and carrier - useful for in vivo imaging of amyloid deposits, for
XX diagnosing Alzheimer's disease and Down's Syndrome.

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XX
XX Example 1; Page 23; 58pp; English.
XX
XX AAR64170, the A4-O(1-28) polypeptide is the first 28 amino acids of the
XX 4.2 kD peptide deriv. from senile plaque cores of an AD (Alzheimer's
XX disease) brain. Known as beta amyloid. A4-O has strong aggregation
XX properties, and binds to itself strongly. This peptide is used to obtain
XX and select beta amyloid proteins that can be used for in vivo imaging
XX of amyloid deposits and hence diagnosis of an amyloidosis-associated
XX disease, such as AD or Down's syndrome. AAR64165 shows the generic
XX sequence of the amyloid protein for generation of variants.
XX
XX Sequence 28 AA:
SQ
XX
XX Query Match 100.0%; Score 55; DB 16; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 0.00044;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHOKLVFFAE 10
XX | | | | | | | |
XX 13 HHOKLVFFAE 22
DB
XX
XX RESULT 22
XX AAR64171
XX ID AAR64171 standard; peptide; 28 AA.
XX
XX AAR64171;
XX
XX 03-AUG-1995 (first entry)
XX
XX A4-P(1-28) a partial beta amyloid peptide.
XX
XX beta amyloid protein; mutant; variant; detection; amyloid deposition;
XX diagnosis; amyloidosis associated disease; Alzheimer's disease;
XX Down's syndrome; A4-P(1-28).
XX
XX Synthetic.
XX
XX W09428412-A.
XX
XX 08-DEC-1994.
XX
XX 27-MAY-1994; 94WO-US05809.
XX
XX 28-MAY-1993; 93US-0069010.
XX
XX (MIRI-) MIRIAM HOSPITAL.
XX
XX Majocha RE, Marotta CA;
XX
XX WPI; 1995-023013/03.
XX
XX Amyloid binding composition comprising labelled amyloid protein
XX and carrier - useful for in vivo imaging of amyloid deposits, for
XX diagnosing Alzheimer's disease and Down's Syndrome.
XX
XX Example 3; Page 23; 58pp; English.
XX
XX AAR64171, the A4-P(1-28) polypeptide is deriv. from vascular amyloid of
XX the AD (Alzheimer's disease) brain and a Down Syndrome brain. Three of
XX the 28 amino acids are different from the A4-O(1-28) peptide shown in
XX AAR64170. A4-O has strong aggregation properties, and binds to itself
XX strongly. It is used to obtain and select beta amyloid proteins that can
XX be used for in vivo imaging of amyloid deposits and hence diagnosis of
XX an amyloidosis-associated disease, such as AD or Down's syndrome.
XX AAR64165 shows the generic sequence of the amyloid protein for generation
XX of variants.
XX
XX Sequence 28 AA:
SQ
XX
XX Query Match 100.0%; Score 55; DB 16; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 0.00044;

```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
 |||||
 DB 13 HHOKLVFFAE 22

RESULT 23
 AAR64172
 ID AAR64172 standard; peptide; 28 AA.
 AC AAR64172;
 XX
 DT 03-AUG-1995 (first entry)
 XX
 DE A4-B(1-28) a partial beta amyloid peptide.
 XX
 KM beta amyloid protein; mutant; variant; detection; amyloid deposition;
 KM diagnosis; amyloidosis associated disease; Alzheimer's disease;
 KM Down's syndrome; A4-B(1-28).
 XX
 OS Synthetic.
 XX
 PN WO9428412-A.
 XX
 PD 08-DEC-1994.
 XX
 PF 27-MAY-1994; 94WO-US05809.
 XX
 PR 28-MAY-1993; 93US-0069010.
 XX
 PA (MIRI-) MIRIAM HOSPITAL.
 XX
 PI Majocha RE, Marotta CA;
 XX
 DR WPI; 1995-023013/03.
 XX
 PT Amyloid binding composition comprising labelled amyloid protein
 PT and carrier - useful for in vivo imaging of amyloid deposits, for
 PT diagnosing Alzheimer's disease and Down's Syndrome.
 XX
 PS Example 3; Page 23; 58pp; English.
 XX
 CC AAR64172, the A4-B(1-28) polypeptide is deriv. from vascular amyloid of
 CC the AD (Alzheimer's disease) brain and a Down Syndrome brain. Three of
 CC the 28 amino acids are different from the A4-O(1-28) peptide shown in
 CC AAR64170. A4-O has strong aggregation properties, and binds to itself
 CC strongly. It is used to obtain and select beta amyloid proteins that can
 CC be used for in vivo imaging of amyloid deposits and hence diagnosis of
 CC an amyloidosis-associated disease, such as AD or Down's syndrome.
 CC AAR64165 shows the generic sequence of the amyloid protein for generation
 CC of variants.
 XX
 SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 16; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
 |||||
 DB 13 HHOKLVFFAE 22

RESULT 24
 AAR64164
 ID AAR64164 standard; peptide; 28 AA.
 AC AAR64164;
 XX
 DT 02-AUG-1995 (first entry)
 XX
 DE Generic beta amyloid protein variant.

XX generic sequence; beta amyloid protein; mutant; variant; detection;
 KM amyloid deposition; diagnosis; amyloidosis associated disease;
 KM Alzheimer's disease; Down's syndrome.
 XX
 OS Synthetic.
 XX
 PN Key Location/Qualifiers
 FT Misc-difference 11 /note- "Glu or Gln"
 FT Misc-difference 27 /note- "Ser or Asn"
 FT Misc-difference 28 /note- "Ala or Lys"
 XX
 PN WO9428412-A.
 XX
 PD 08-DEC-1994.
 XX
 PF 27-MAY-1994; 94WO-US05809.
 XX
 PR 28-MAY-1993; 93US-0069010.
 XX
 PA (MIRI-) MIRIAM HOSPITAL.
 XX
 PI Majocha RE, Marotta CA;
 XX
 DR WPI; 1995-023013/03.
 XX
 PT Amyloid binding composition comprising labelled amyloid protein
 PT and carrier - useful for in vivo imaging of amyloid deposits, for
 PT diagnosing Alzheimer's disease and Down's Syndrome.
 XX
 PS Claim 3; Page 42; 58pp; English.
 XX
 CC AAR64164 shows the generic amino acid sequence of a variant beta amyloid
 CC protein. The protein binds amyloid and is useful for in vivo imaging of
 CC amyloid deposits and hence diagnosis of an amyloidosis-associated
 CC disease, such as Alzheimer's disease or Down's syndrome. AAR64165-69
 CC show specific variants generated from this generic sequence with addition
 CC amino acids.
 XX
 SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 16; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
 |||||
 DB 13 HHOKLVFFAE 22

RESULT 25
 AAM01413
 ID AAM01413 standard; Protein; 28 AA.
 AC AAM01413;
 XX
 DT 20-JAN-1997 (first entry)
 XX
 DE Beta/A4-amyloid peptide residues 1-28.
 XX
 KM Beta/A4-amyloid peptide; tissue plasminogen activator;
 KM Alzheimer's disease; stimulation; investigation; pathogenesis;
 KM hereditary cerebral haemorrhage with amyloidosis-dutch type;
 KM control; cerebral amyloid angiopathy; cerebral; haemorrhage;
 KM hemorrhage.
 XX
 OS Homo sapiens.
 XX
 PN WO9615799-A1.

PD 30-MAY-1996.
 XX
 XX 22-NOV-1995; 95MO-US15007.
 PF
 XX
 PR 22-NOV-1994; 94US-0347144.
 XX
 PA (RUT) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Anderson S;
 XX
 DR WPI; 1996-268332/27.
 XX
 PT Use of agents which bind beta-amyloid peptide - for diagnosis,
 PT prevention and treatment of vascular damage caused by amyloid
 PT deposits, partic. in haemorrhaging and Alzheimer's disease
 XX
 PS Example 1; Fig 1; 52pp; English.
 XX
 CC To investigate the effects of beta-amyloid peptide (BAP) on
 CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.
 CC One peptide contained 42 amino acids and corresp. to the full
 CC length BAP (AAR95248). The other 2 peptides (AAR95249 and 50) contained
 CC the 28 N-terminal residues of the BAP found in Alzheimer's disease
 CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type
 CC (HCHWA-D), respectively. In an assay to determine the effect of
 CC the peptides on t-PA activation, each peptide (AAR95248, 49 and 50)
 CC gave 1st order rate constant of activation (k_{app}) values of
 CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null
 CC and fibrinogen controls. The results demonstrate that the BAP are
 CC able to stimulate t-PA activity in vitro, which is significant in
 CC that it provides a means for investigating and controlling the
 CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
 CC angiopathy related cerebral haemorrhage.
 XX
 SQ Sequence 28 AA;
 XX
 QY 1 HHOKLVFFAE 10
 DB 13 HHOKLVFFAE 22

Query Match 100.0%; Score 55; DB 17; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 26
 AAY39805
 ID AAY39805 standard; peptide; 28 AA.
 XX
 AC AAY39805;
 XX
 DT 29-NOV-1999 (first entry)
 XX
 DE Beta-amyloid protein, Beta/A4 amyloid (1-28).
 XX
 KW Beta-amyloid protein; Alzheimer's disease; amyloidosis; joint swelling;
 KW long-standing inflammation; malignancy; Familial Mediterranean Fever;
 KW multiple myeloma; plasma cell dyscrasia; long-term haemodialysis; kuru;
 KW carpal tunnel syndrome; multiple spontaneous fracture; radiolucency;
 KW endocrine tumour; medullary carcinoma; Down's syndrome; scrapie;
 KW Creutzfeldt-Jakob disease; Gerstmann Strausler Syndrome;
 KW subacute spongiform encephalopathy; therapy.
 XX
 OS Homo sapiens.
 XX
 PN US5958883-A.
 XX
 PD 28-SEP-1999.
 XX
 PF 05-JUN-1995; 95US-0461216.
 XX
 PR 23-OCT-1992; 92US-0969734.
 PR 23-SEP-1992; 92US-0950417.

XX
 PA (UNIV) UNIV WASHINGTON.
 XX
 PI Snow AD;
 XX
 DR WPI; 1999-561062/47.
 XX
 PT Peptides of 6-8 amino acids useful for treating or preventing
 PT amyloidosis -
 XX
 PS Disclosure; Column 67-68; 83pp; English.
 XX
 CC This sequence represents a fragment of the beta-amyloid protein. The
 CC invention relates to a method for treating or preventing a form of
 CC amyloidosis, including Alzheimer's disease using this sequence. The
 CC compositions may be useful for treating or preventing the amyloidosis
 CC associated with long-standing inflammation, various forms of malignancy
 CC (including B-cell type malignancies), Familial Mediterranean Fever,
 CC multiple myeloma, plasma cell dyscrasias, long-term haemodialysis, carpal
 CC tunnel syndrome, joint swelling, multiple spontaneous fractures,
 CC radiolucency in the wrist and hip, endocrine tumours, medullary carcinoma
 CC of the thyroid, diabetes, Alzheimer's disease, Down's syndrome, scrapie
 CC Creutzfeldt-Jakob disease, Gerstmann Strausler Syndrome, kuru, scrapie
 CC and other subacute spongiform encephalopathies.
 XX
 SQ Sequence 28 AA;
 XX
 QY 1 HHOKLVFFAE 10
 DB 13 HHOKLVFFAE 22

Query Match 100.0%; Score 55; DB 20; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 27
 AAM81467
 ID AAM81467 standard; peptide; 28 AA.
 XX
 AC AAM81467;
 XX
 DT 28-JAN-1999 (first entry)
 XX
 DE Synthetic amyloid beta (Abeta) peptide 2 (residues 1-28).
 XX
 KW Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
 KW research; neurotoxicity; free-radical; glutamine synthetase.
 XX
 OS Synthetic.
 XX
 PN US5840838-A.
 XX
 PD 24-NOV-1998.
 XX
 PF 29-FEB-1996; 96US-0609090.
 XX
 PR 29-FEB-1996; 96US-0609090.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 PI Aksenov M, Butterfield DA, Carney JM, Hensley K;
 XX
 DR WPI; 1999-034120/03.
 XX
 PT Process for treating synthetic amyloid beta peptides - by organic
 PT solvent treatment, useful for studying neurotoxicity
 XX
 PS Claim 5; Columns 9-10; 14pp; English.
 XX
 CC Sequences AAM81466 to AAM81476 represent synthetic amyloid beta (Abeta)
 CC peptides. The invention provides a process for treating a synthetic
 CC Abeta peptide that comprises dissolving the peptide in a deoxygenated

CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
 CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
 CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
 CC 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta
 CC peptides are useful as research tools for studying neurotoxicity
 CC resulting from Abeta peptide -enhanced free-radical production. The
 CC treatment increases the activity of the synthetic Abeta peptides in tests
 CC to determine free-radical generating capacity and glutamine synthetase
 CC inactivation.

CC Sequence 28 AA;

Query Match 100.0%; Score 55; DB 20; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00044;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
 Db 13 HHOKLVFFAE 22

RESULT 28

AAB91783
 ID AAB91783 standard; Peptide: 28 AA.

XX AAB91783;

DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:959.

KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimide; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
 OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONU-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

PT WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 507; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

CC Sequence 28 AA;

Query Match 100.0%; Score 55; DB 22; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00044;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
 Db 13 HHOKLVFFAE 22

RESULT 29

AAB91789
 ID AAB91789 standard; Peptide: 28 AA.

XX AAB91789;

DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:965.

KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimide; maleimido group; amino;
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
 OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONU-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

PT WPI; 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 509; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX Sequence 28 AA; Score 55; DB 22; Length 28;
 Query Match 100.0%; Pred. No. 0.00044;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
 |||||
 Db 13 HHOKLVFFAE 22

RESULT 30
 AAB91800
 ID AAB91800 standard; Peptide; 28 AA.
 AC AAB91800;
 DT 22-JUN-2001 (first entry)
 DE Amyloid beta-protein fragment peptide SEQ ID NO:976.
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimide; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200069900-A2.
 PD 23-NOV-2000.
 PF 17-MAY-2000; 2000WO-US13576.
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 PA (CONJ-) CONJUCHEM INC.
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 DR WPI; 2001-112059/12.
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PS Disclosure; Page 513; 733pp; English.
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX Sequence 28 AA;

Query Match 100.0%; Score 55; DB 22; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00044;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHOKLVFFAE 10
 |||||
 Db 13 HHOKLVFFAE 22

RESULT 31
 AAB91816
 ID AAB91816 standard; Peptide; 28 AA.
 AC AAB91816;
 DT 22-JUN-2001 (first entry)
 DE Amyloid beta-protein fragment peptide SEQ ID NO:992.
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KM blood component; modification; succinimide; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200069900-A2.
 PD 23-NOV-2000.
 PF 17-MAY-2000; 2000WO-US13576.
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 PA (CONJ-) CONJUCHEM INC.
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 DR WPI; 2001-112059/12.
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PS Disclosure; Page 519; 733pp; English.
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX Sequence 28 AA;

Query Match 100.0%; Score 55; DB 22; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
PF 02-SEP-1999; 99US-0388890.
XX
XX 26-JUL-1996; 96US-0686959.
PR 22-NOV-1994; 94US-0347144.
PR 22-NOV-1995; 95WO-US15007.
XX
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX Anderson S;
XX
XX WPI; 2001-030939/04.
XX
XX
XX Identifying mutant tissue-type plasminogen activator (t-PA) for
XX improving thrombolytic therapy or treating vascular hemorrhaging, by
XX determining whether t-PA binds to fibrin but not to a beta amyloid
XX peptide
XX
XX Example 3; Column 26; 23pp; English.
XX
XX The present invention describes a method for identifying mutant
XX derivatives of tissue-type plasminogen activator, which involves
XX determining whether or not they bind to beta-amyloid peptides and fibrin.
XX Mutants will only bind to the latter. These mutants are useful in
XX improved thrombolytic therapies, in the treatment of Alzheimer's disease
XX and in the treatment of acute cardiovascular disease, which may be caused
XX by myocardial infarction, stroke, ischemia and pulmonary embolism.
XX
XX Sequence 28 AA;
XX
XX Query Match 100.0%; Score 55; DB 22; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 0.00044;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HHOKLVEFAE 10
XX |||||
XX Db 13 HHOKLVEFAE 22
XX
XX RESULT 35
XX AAB35591
XX ID AAB35591 standard; peptide; 28 AA.
XX
XX AC AAB35591;
XX
XX DT 15-FEB-2001 (first entry)
XX
XX DE Human clone D1N B(1-28) amyloid B peptide.
XX
XX KW Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
XX acute cardiovascular disease; therapy.
XX
XX OS Homo sapiens.
XX
XX PN US6136548-A.
XX
XX PD 24-OCT-2000.
XX
XX PF 02-SEP-1999; 99US-0388890.
XX
XX PR 26-JUL-1996; 96US-0686959.
XX 22-NOV-1994; 94US-0347144.
XX 22-NOV-1995; 95WO-US15007.
XX
XX PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX PI Anderson S;
XX
XX WPI; 2001-030939/04.
XX
XX
XX Identifying mutant tissue-type plasminogen activator (t-PA) for
XX improving thrombolytic therapy or treating vascular hemorrhaging, by
XX determining whether t-PA binds to fibrin but not to a beta amyloid
XX peptide
```

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XX
XX Example 3; Column 26; 23pp; English.
XX
XX The present invention describes a method for identifying mutant
XX derivatives of tissue-type plasminogen activator, which involves
XX determining whether or not they bind to beta-amyloid peptides and fibrin.
XX Mutants will only bind to the latter. These mutants are useful in
XX improved thrombolytic therapies, in the treatment of Alzheimer's disease
XX and in the treatment of acute cardiovascular disease, which may be caused
XX by myocardial infarction, stroke, ischemia and pulmonary embolism.
XX
XX Sequence 28 AA;
XX
XX Query Match 100.0%; Score 55; DB 22; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 0.00044;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 HHOKLVEFAE 10
XX |||||
XX Db 13 HHOKLVEFAE 22
XX
XX RESULT 36
XX AAB35592
XX ID AAB35592 standard; peptide; 28 AA.
XX
XX AC AAB35592;
XX
XX DT 15-FEB-2001 (first entry)
XX
XX DE Human clone E3Q B(1-28) amyloid B peptide.
XX
XX KW Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
XX acute cardiovascular disease; therapy.
XX
XX OS Homo sapiens.
XX
XX PN US6136548-A.
XX
XX PD 24-OCT-2000.
XX
XX PF 02-SEP-1999; 99US-0388890.
XX
XX PR 26-JUL-1996; 96US-0686959.
XX 22-NOV-1994; 94US-0347144.
XX 22-NOV-1995; 95WO-US15007.
XX
XX PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
XX
XX PI Anderson S;
XX
XX WPI; 2001-030939/04.
XX
XX
XX Identifying mutant tissue-type plasminogen activator (t-PA) for
XX improving thrombolytic therapy or treating vascular hemorrhaging, by
XX determining whether t-PA binds to fibrin but not to a beta amyloid
XX peptide
XX
XX Example 3; Column 26; 23pp; English.
XX
XX The present invention describes a method for identifying mutant
XX derivatives of tissue-type plasminogen activator, which involves
XX determining whether or not they bind to beta-amyloid peptides and fibrin.
XX Mutants will only bind to the latter. These mutants are useful in
XX improved thrombolytic therapies, in the treatment of Alzheimer's disease
XX and in the treatment of acute cardiovascular disease, which may be caused
XX by myocardial infarction, stroke, ischemia and pulmonary embolism.
XX
XX Sequence 28 AA;
XX
XX Query Match 100.0%; Score 55; DB 22; Length 28;
XX Best Local Similarity 100.0%; Pred. No. 0.00044;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 HHOKLVFFAE 10
 |||||
 DB 13 HHOKLVFFAE 22

RESULT 37
 AAB35593
 ID AAB35593 standard; peptide; 28 AA.

AC AAB35593;

DT 15-FEB-2001 (first entry)

DE Human clone R5Q B(1-28) amyloid B peptide.

KW Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
 acute cardiovascular disease; therapy.

OS Homo sapiens.

PN US6136548-A.

PD 24-OCT-2000.

PF 02-SEP-1999; 99US-0388890.

PR 26-JUL-1996; 96US-0686959.

PR 22-NOV-1994; 94US-0347144.

PR 22-NOV-1995; 95WO-US15007.

PA (RUTE) UNIV RUTGERS STATE NEW JERSEY.

PI Anderson S;

DR WPI; 2001-030939/04.

PT Identifying mutant tissue-type plasminogen activator (t-PA) for
 PT improving thrombolytic therapy or treating vascular hemorrhaging, by
 PT determining whether t-PA binds to fibrin but not to a beta amyloid
 PT peptide

PS Example 3; Column 26; 23pp; English.

CC The present invention describes a method for identifying mutant
 CC derivatives of tissue-type plasminogen activator, which involves
 CC determining whether or not they bind to beta-amyloid peptides and fibrin.
 CC Mutants will only bind to the latter. These mutants are useful in
 CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
 CC and in the treatment of acute cardiovascular disease, which may be caused
 CC by myocardial infarction, stroke, ischaemia and pulmonary embolism.

SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 22; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.00044;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
 |||||
 DB 13 HHOKLVFFAE 22

RESULT 38
 AAB35594

ID AAB35594 standard; peptide; 28 AA.

AC AAB35594;

DT 15-FEB-2001 (first entry)

DE Human clone H6Q B(1-28) amyloid B peptide.

KW Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
 KW acute cardiovascular disease; therapy.

OS Homo sapiens.

PN US6136548-A.

PD 24-OCT-2000.

PF 02-SEP-1999; 99US-0388890.

PR 26-JUL-1996; 96US-0686959.

PR 22-NOV-1994; 94US-0347144.

PR 22-NOV-1995; 95WO-US15007.

PA (RUTE) UNIV RUTGERS STATE NEW JERSEY.

PI Anderson S;

DR WPI; 2001-030939/04.

PT Identifying mutant tissue-type plasminogen activator (t-PA) for
 PT improving thrombolytic therapy or treating vascular hemorrhaging, by
 PT determining whether t-PA binds to fibrin but not to a beta amyloid
 PT peptide

PS Example 3; Column 26; 23pp; English.

CC The present invention describes a method for identifying mutant
 CC derivatives of tissue-type plasminogen activator, which involves
 CC determining whether or not they bind to beta-amyloid peptides and fibrin.
 CC Mutants will only bind to the latter. These mutants are useful in
 CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
 CC and in the treatment of acute cardiovascular disease, which may be caused
 CC by myocardial infarction, stroke, ischaemia and pulmonary embolism.

SQ Sequence 28 AA;

Query Match 100.0%; Score 55; DB 22; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.00044;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAE 10
 |||||
 DB 13 HHOKLVFFAE 22

RESULT 39
 AAB35595
 ID AAB35595 standard; peptide; 28 AA.

AC AAB35595;

DT 15-FEB-2001 (first entry)

DE Human clone D7Q B(1-28) amyloid B peptide.

KW Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
 KW acute cardiovascular disease; therapy.

OS Homo sapiens.

PN US6136548-A.

PD 24-OCT-2000.

PF 02-SEP-1999; 99US-0388890.

PR 26-JUL-1996; 96US-0686959.

PR 22-NOV-1994; 94US-0347144.

PR 22-NOV-1995; 95WO-US15007.

PA (RUTE) UNIV RUTGERS STATE NEW JERSEY.

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XX  Anderson S;
PI  WPI; 2001-030939/04.
DR  Identifying mutant tissue-type plasminogen activator (t-PA) for
XX  improving thrombolytic therapy or treating vascular hemorrhaging, by
PT  determining whether t-PA binds to fibrin but not to a beta amyloid
PT  peptide
XX  Example 3; Column 26; 23pp; English.
XX  The present invention describes a method for identifying mutant
CC  derivatives of tissue-type plasminogen activator, which involves
CC  determining whether or not they bind to beta-amyloid peptides and fibrin.
CC  Mutants will only bind to the latter. These mutants are useful in
CC  improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC  and in the treatment of acute cardiovascular disease, which may be caused
CC  by myocardial infarction, stroke, ischemia and pulmonary embolism.
XX  Sequence 28 AA;
SQ
Query Match 100.0%; Score 55; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22
RESULTS 40
AAB35596
ID AAB35596 standard; peptide; 28 AA.
AC AAB35596;
XX 15-FEB-2001 (first entry)
DT Human clone E11Q B(1-28) amyloid B peptide.
XX 15-FEB-2001 (first entry)
DE Human clone E11Q B(1-28) amyloid B peptide.
XX Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KM acute cardiovascular disease; therapy.
XX Homo sapiens.
OS
XX US6136548-A.
XX 24-OCT-2000.
PD
XX 02-SEP-1999; 99US-0388890.
PF
XX 26-JUL-1996; 96US-0686959.
PR 22-NOV-1994; 94US-0347144.
PR 22-NOV-1995; 95WO-US15007.
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
PA
XX Anderson S;
PI
XX WPI; 2001-030939/04.
DR Identifying mutant tissue-type plasminogen activator (t-PA) for
XX improving thrombolytic therapy or treating vascular hemorrhaging, by
PT determining whether t-PA binds to fibrin but not to a beta amyloid
PT peptide
XX Example 3; Column 26; 23pp; English.
XX The present invention describes a method for identifying mutant
CC derivatives of tissue-type plasminogen activator, which involves
CC determining whether or not they bind to beta-amyloid peptides and fibrin.
CC Mutants will only bind to the latter. These mutants are useful in
CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC and in the treatment of acute cardiovascular disease, which may be caused
CC by myocardial infarction, stroke, ischemia and pulmonary embolism.
XX Sequence 28 AA;
SQ
Query Match 100.0%; Score 55; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22
RESULTS 42

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CC Improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC and in the treatment of acute cardiovascular disease, which may be caused
CC by myocardial infarction, stroke, ischemia and pulmonary embolism.
XX Sequence 28 AA;
SQ
Query Match 100.0%; Score 55; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22
RESULTS 41
AAB36201
ID AAB36201 standard; peptide; 28 AA.
AC AAB36201;
XX 15-FEB-2001 (first entry)
DT Human clone D23Q B(1-28) amyloid B peptide.
XX 15-FEB-2001 (first entry)
DE Human clone D23Q B(1-28) amyloid B peptide.
XX Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
KM acute cardiovascular disease; therapy.
XX Homo sapiens.
OS
XX US6136548-A.
XX 24-OCT-2000.
PD
XX 02-SEP-1999; 99US-0388890.
PF
XX 26-JUL-1996; 96US-0686959.
PR 22-NOV-1994; 94US-0347144.
PR 22-NOV-1995; 95WO-US15007.
XX (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
PA
XX Anderson S;
PI
XX WPI; 2001-030939/04.
DR Identifying mutant tissue-type plasminogen activator (t-PA) for
XX improving thrombolytic therapy or treating vascular hemorrhaging, by
PT determining whether t-PA binds to fibrin but not to a beta amyloid
PT peptide
XX Example 3; Column 26; 23pp; English.
XX The present invention describes a method for identifying mutant
CC derivatives of tissue-type plasminogen activator, which involves
CC determining whether or not they bind to beta-amyloid peptides and fibrin.
CC Mutants will only bind to the latter. These mutants are useful in
CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC and in the treatment of acute cardiovascular disease, which may be caused
CC by myocardial infarction, stroke, ischemia and pulmonary embolism.
XX Sequence 28 AA;
SQ
Query Match 100.0%; Score 55; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22
RESULTS 42

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AAB36202
 ID AAB36202 standard; peptide; 28 AA.
 XX
 AC AAB36202;
 XX
 DT 15-FEB-2001 (first entry)
 XX
 DE Human clone K28Q B(1-28) amyloid B peptide.
 XX
 KM Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
 KM acute cardiovascular disease; therapy.
 XX
 OS Homo sapiens.
 XX
 PN US6136548-A.
 XX
 PD 24-OCT-2000.
 XX
 PF 02-SEP-1999; 99US-0388890.
 XX
 PR 26-JUL-1996; 96US-0686959.
 PR 22-NOV-1994; 94US-0347144.
 PR 22-NOV-1995; 95WO-US15007.
 XX
 PA (RUTE) UNIV ROTGERS STATE NEW JERSEY.
 XX
 PI Anderson S;
 XX
 DR WPI; 2001-030939/04.
 XX
 PT Identifying mutant tissue-type plasminogen activator (t-PA) for
 PT improving thrombolytic therapy or treating vascular hemorrhaging, by
 PT determining whether t-PA binds to fibrin but not to a beta amyloid
 PT peptide
 XX
 PS Example 3; Column 26; 23pp; English.
 XX
 CC The present invention describes a method for identifying mutant
 CC derivatives of tissue-type plasminogen activator, which involves
 CC determining whether or not they bind to beta-amyloid peptides and fibrin.
 CC Mutants will only bind to the latter. These mutants are useful in
 CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
 CC and in the treatment of acute cardiovascular disease, which may be caused
 CC by myocardial infarction, stroke, ischemia and pulmonary embolism.
 CC
 XX
 SQ Sequence 28 AA;
 XX
 Query Match 100.0%; Score 55; DB 22; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHOKLVFFAE 10
 DB 13 HHOKLVFFAE 22
 XX
 RESULT 43
 ID AAW81468 standard; peptide; 30 AA.
 XX
 AC AAW81468;
 XX
 DT 28-JAN-1999 (first entry)
 XX
 DE Synthetic amyloid beta (Abeta) peptide 3 (residues 1-30).
 XX
 KM Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
 KM research; neurotoxicity; free-radical; glutamine synthetase.
 XX
 OS Synthetic.
 XX
 PN US5840838-A.
 XX

PD 24-NOV-1998.
 XX
 PF 29-FEB-1996; 96US-0609090.
 XX
 PR 29-FEB-1996; 96US-0609090.
 XX
 PA (KENT) UNIV KENTUCKY RES FOUND.
 XX
 PI Aksekov M, Butterfield DA, Carney JM, Hensley K;
 PI WPI; 1999-034120/03.
 DR
 XX
 PT Process for treating synthetic amyloid beta peptides - by organic
 PT solvent treatment, useful for studying neurotoxicity
 XX
 PS Claim 5; Columns 9-10; 14pp; English.
 XX
 CC Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
 CC peptides. The invention provides a process for treating a synthetic
 CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
 CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
 CC sulfoxide, morpholinopropanesulphonic acid, dimethylformamide and
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
 CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
 CC 'evaporative deposition' in 5-10 minutes. Synthetic amyloid beta
 CC peptides are useful as research tools for studying neurotoxicity
 CC resulting from Abeta peptide -enhanced free-radical production. The
 CC treatment increases the activity of the synthetic Abeta peptides in tests
 CC to determine free-radical generating capacity and glutamine synthetase
 CC inactivation.
 XX
 SQ Sequence 30 AA;
 XX
 Query Match 100.0%; Score 55; DB 20; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.00047;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHOKLVFFAE 10
 DB 13 HHOKLVFFAE 22
 XX
 RESULT 44
 ID AAB84430 standard; peptide; 32 AA.
 XX
 AC AAB84430;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Partial sequence of a human beta-amyloid precursor protein.
 XX
 KM Beta-amyloid precursor protein; APP; chimeric peptide; B cell epitope;
 KM vaccine.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT Modified-site 1 /note="pyroglutamate"
 XX
 PN WO200142306-A2.
 XX
 PD 14-JUN-2001.
 XX
 PF 08-DEC-2000; 2000WO-US33203.
 XX
 PR 08-DEC-1999; 99US-0169687.
 XX
 PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.
 XX
 PI Chain B;
 XX

Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

RESULT 47

AAW89357
ID AAW89357 standard; peptide; 35 AA.

AC AAW89357;

DT 02-MAR-1999 (first entry)

DE Beta-amyloid peptide derivative A-beta-6-40.

KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polynuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; bAP.

OS Homo sapiens.
OS Synthetic.

PN US5854204-A.

PD 29-DEC-1998.

PF 14-MAR-1996; 96US-0612785.

PR 14-MAR-1996; 96US-0612785.

PR 14-MAR-1995; 95US-0404831.

PR 07-JUN-1995; 95US-0475579.

PR 27-OCT-1995; 95US-0548998.

PA (PRAE-) PRAECIS PHARM INC.

PI Benjamin H, Chin J, Findels MA, Garnick MB, Gelter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
DR WPI: 1999-094964/08.

PT New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease

PS Claim 5; Column 81-82; 52pp; English.

CC The present invention describes beta-amyloid peptide (bAP) derivatives.
CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically bAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of bAP to
CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
CC even when bAP is present in molar excess. The present sequence
CC represents a bAP derivative.

SQ Sequence 35 AA;

Query Match 100.0%; Score 55; DB 20; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 8 HHOKLVFFAE 17

RESULT 48

AAW89359
ID AAW89359 standard; peptide; 35 AA.

AC AAW89359;

DT 02-MAR-1999 (first entry)

DE Beta-amyloid peptide derivative A-beta-1-25,31-40 (Delta26-30).

KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polynuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; bAP.

OS Homo sapiens.
OS Synthetic.

PN US5854204-A.

PD 29-DEC-1998.

PF 14-MAR-1996; 96US-0612785.

PR 14-MAR-1996; 96US-0612785.

PR 14-MAR-1995; 95US-0404831.

PR 07-JUN-1995; 95US-0475579.

PR 27-OCT-1995; 95US-0548998.

PA (PRAE-) PRAECIS PHARM INC.

PI Benjamin H, Chin J, Findels MA, Garnick MB, Gelter ML;
PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
DR WPI: 1999-094964/08.

PT New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease

PS Claim 7; Column 81-82; 52pp; English.

CC The present invention describes beta-amyloid peptide (bAP) derivatives.
CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically bAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of bAP to
CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
CC even when bAP is present in molar excess. The present sequence
CC represents a bAP derivative.

SQ Sequence 35 AA;

Query Match 100.0%; Score 55; DB 20; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHOKLVFFAE 10
DB 13 HHOKLVFFAE 22

RESULT 49

AAW89361
ID AAW89361 standard; peptide; 35 AA.

AC AAW89361;

DF 02-MAR-1999 (first entry)
 XX Beta-amyloid peptide derivative A-beta-1-5,11-40 (Delta6-10).
 DE
 XX Human: beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
 KM aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
 KM familial amyloid polyneuropathy; bovine spongiform encephalopathy;
 KM Creutzfeldt-Jakob disease; bap.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US5854204-A.
 PD 29-DEC-1998.
 XX
 PF 14-MAR-1996; 96US-0612785.
 XX
 PR 14-MAR-1996; 96US-0612785.
 PR 14-MAR-1995; 95US-0404831.
 PR 07-JUN-1995; 95US-0475579.
 PR 27-OCT-1995; 95US-0548998.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PI Benjamin H, Chin J, Findels MA, Garnick MB, Gelfer ML;
 PI Hundal A, Kasman L, Kelley M, Kudasek W, Lee J;
 PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
 DR WPI; 1999-094964/08.
 XX
 PT New peptide(s) derived from beta-amyloid peptide that inhibit
 PT amyloid aggregation - and neurotoxicity, specifically for treatment
 PT and prevention of Alzheimer's disease
 XX
 PS Claim 9; Column 83-84; 52pp; English.
 CC The present invention describes beta-amyloid peptide (bap) derivatives.
 CC The bap derivatives inhibit aggregation of amyloidogenic proteins and
 CC peptides, specifically bap, and their neurotoxicity, so are useful for
 CC treating and preventing any disease involving amyloidosis, specifically
 CC Alzheimer's disease but also Down's syndrome, familial amyloid
 CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
 CC Creutzfeldt-Jakob disease. The bap derivatives are also used to diagnose
 CC these diseases, in vitro or in vivo, by detecting binding of bap to
 CC labelled bap derivatives. Some bap derivatives inhibit bap aggregation
 CC even when bap is present in molar excess. The present sequence
 CC represents a bap derivative.
 XX
 SQ Sequence 35 AA:
 Query Match 100.0%; Score 55; DB 20; Length 35;
 Best Local Similarity 100.0%; Pred. No. 0.00056;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHOKLVFFAE 10
 DB 8 HHOKLVFFAE 17
 RESULT 50
 AAW81471
 ID AAW81471 standard; peptide; 36 AA.
 XX
 AC AAW81471;
 XX
 DF 28-JAN-1999 (first entry)
 XX
 DE Synthetic amyloid beta (Abeta) peptide 6 (residues 1-36).
 KM Amyloid beta; Abeta; deoxygenated solvent; evaporative deposition;
 KM research; neurotoxicity; free-radical; glutamine synthetase.
 XX

OS Synthetic.
 PN US5840838-A.
 XX
 PD 24-NOV-1998.
 XX
 PF 29-FEB-1996; 96US-0609090.
 XX
 PR 29-FEB-1996; 96US-0609090.
 XX
 PA (KENT) UNIV KENTUCKY RES. FOUND.
 PI Aksenov M, Butterfield DA, Carney JM, Hensley K;
 DR WPI; 1999-034120/03.
 XX
 PT Process for treating synthetic amyloid beta peptides - by organic
 PT solvent treatment, useful for studying neurotoxicity
 XX
 PS Claim 5; Columns 11-12; 14pp; English.
 CC Sequences AAW81466 to AAW81476 represent synthetic amyloid beta (Abeta)
 CC peptides. The invention provides a process for treating a synthetic
 CC Abeta peptide that comprises dissolving the peptide in a deoxygenated
 CC solvent selected from trifluoroethanol, hexafluorocyclohexane, dimethyl
 CC sulphoxide, morpholinopropanesulphonic acid, dimethylformamide and
 CC acetonitrile to a concentration of 0.01-10 mg/ml, incubating the
 CC solution at 20-65 deg. C for 0.5-4 hour, and removing the solvent by
 CC "evaporative deposition" in 5-10 minutes. Synthetic amyloid beta
 CC peptides are useful as research tools for studying neurotoxicity
 CC resulting from Abeta peptide -enhanced free-radical production. The
 CC treatment increases the activity of the synthetic Abeta peptides in tests
 CC to determine free-radical generating capacity and glutamine synthetase
 CC inactivation.
 XX
 SQ Sequence 36 AA:
 Query Match 100.0%; Score 55; DB 20; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.00057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHOKLVFFAE 10
 DB 13 HHOKLVFFAE 22
 Search completed: October 29, 2002, 09:24:07
 Job time : 33 secs